

# FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCTCGGGGATCCTCTAGAGATCCCTCGACCTCGA  
CCCACGCGTCCGGGCCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCG  
CAGCGCTACCCGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTG  
CTGCTGCCGCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCT  
GGTGGACAAGTTTAAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACA  
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTTCGCTGTGAGATC  
CTGGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA  
GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTTCGAGTGGTTTT  
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGC  
CAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACA  
GGGCGACGGGTCTTGCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGG  
ACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC  
TGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCT  
GGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCCTCCCTGCAGCGCTG  
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTG  
GGCTGCACAGGGGAAGGCCCAGGAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA  
CGGACAGTGTGCAGATGTGGACGAGTGCTCACTAGCAGAAAAAACCTGTGTGAGGAAAAACG  
AAAAGTGTACATACTCCAGGGAGCTACGTCTGTGTGTGTCTTGACGGCTTCGAAGAAACG  
GAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCCGACACAGCT  
GCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTACCCTTTAAATTATTCAGAAGGATGTCC  
CGTGGAATAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGCGGGGAGAGGCTGC  
CTGCTCTCTAACGGTTGATTCTCATTTGTCCCTTAAACAGCTGCATTTCTTGTTGTTCTTA  
AACAGACTTGTATATTTTGATACAGTTCCTTGTAAATAAAATTGACCATTGTAGGTAATCAGG  
AGGAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGC  
TTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCA  
TCACAAATTTACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTC  
ATCAATGTATCTTATCATGTCTGGATCGGGAATTAATTCGGCGCAGCACCATGGCCTGAAAT  
AACCTCTGAAAGAGGAACTTGGTTAGGTACCTTCTGAGGCGGAAAGAACCAGCTGTGGAATG  
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCATGC  
ATCTCAATTAGTCAGCAACCCAGTTTTT

## **FIGURE 2**

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAWEEKTLSKYESSEIRL  
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPDCLACQGGSQRPCSG  
NGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDE  
GACVDVDECAAEPPPCSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKT  
CVRKNENCYNTPGSYVCVCPDGFEEETEDACVPPAEAEATEGESPTQLPSREDL

### **Signal peptide:**

amino acids 1-24

### **N-glycosylation sites.**

amino acids 190-194 and 251-255

### **Glycosaminoglycan attachment sites.**

amino acids 149-153 and 155-159

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 26-30

### **Casein kinase II phosphorylation sites.**

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343  
and 349-353

### **Tyrosine kinase phosphorylation site.**

amino acids 303-310

### **N-myristoylation sites.**

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and  
313-319

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 308-320

### **EGF-like domain cysteine pattern signature.**

amino acids 166-178

### **Leucine zipper pattern.**

amino acids 94-116

### FIGURE 3

CAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTC  
GACCTCGACCCACGCGTCCGCCAGGCCGGGAGGCGACGCGCCAGCCGTCTAAACGGGAACA  
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCG  
GCACGAGGAGTTTTCCCGGCAGCGAGGAGGTCCTGAGCAGCATGGCCCCGGAGGAGCGCCTTC  
CCTGCCGCCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGAGGC  
CGGGCCGCCGAGGAGGAGAGCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCA  
TAGGATTTGAAGAAGATATCCTGATTGTTTCAGAGGGGAAAATGGCACCTTTTACACATGAT  
TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTTAC  
CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATTCTGTCTTGCCTCCCTGGATA  
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGTGCCTCACAAGGCA  
TCAGTTGTTCAAGTTGGTTTCCCATGTCTTGGAAAACAGGATGGGGTGGCAGCATTTGAAGT  
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCCAAACACCTCAAATGCTATCT  
TCTTTAAAACATGTCAACAAGCTGAGTGCCAGGCGGGTGCCGAAATGGAGGCTTTTGTAAT  
GAAAGACGCATCTGCGAGTGTCCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTTG  
TACCCACGATGTATGAATGGTGGACTTTGTGTGACTCCTGGTTTCTGCATCTGCCACCTG  
GATTCTATGGAGTGAACCTGTGACAAAGCAAACCTGCTCAACCACCTGCTTTAATGGAGGGACC  
TGTTTCTACCTGGAAAATGTATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAATCAG  
CAAATGCCCACAACCTGTGAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGTT  
CCAAAGGTTACCAGGGAGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGACAT  
GGAACCTGCCATGAACCCAACAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA  
TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCGCCAGCTCAGGCAGC  
ACACGCCTTCACTTAAAAAGGCCGAGGAGCGGCGGGATCCACCTGAATCCAATTACATCTGG  
TGAACTCCGACATCTGAAACGTTTTAAGTTACACCAAGTTCATAGCCTTTGTTAACCTTTCA  
TGTGTTGAATGTTCAAATAATGTTCAATTACACTTAAGAATACTGGCCTGAATTTTATTAGCT  
TCATTATAAATCACTGAGCTGATATTTACTCTTCCTTTTAAAGTTTTCTAAGTACGTCTGTAG  
CATGATGGTATAGATTTTCTTGTTTCAGTGCTTTGGGACAGATTTTATATTATGTCAATTGA  
TCAGGTAAAAATTTTCAGTGTGTAGTTGGCAGATATTTTCAAATTACAATGCATTTATGGT  
GTCTGGGGGCAGGGGAACATCAGAAAGGTTAAATTGGGCAAAAATGCGTAAGTCACAAGAAT  
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTTCAATTTTATTGTGATATTTAGAT  
GTTTGTTACATTTTTTAAAAATTGCTCTTAATTTTTTAACTCTCAATACAATATATTTTGACC  
TTACCATTATTCCAGAGATTCAGTATTAATAAAAAAAAAAATTACACTGTGGTAGTGGCATTT  
AAACAATATAATATATTCTAAACACAATGAAATAGGGAATATAATGTATGAACTTTTTGCA  
TGGCTTGAAGCAATATAATATATTGTAAACAAAACACAGCTCTTACCTAATAAACATTTTAT  
ACTGTTTGTATGTATAAAATAAAGGTGCTGCTTTAGTTTTTTTGGAATAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGCTTGGC  
CGCCATGGCCCAACTTGTTTATTGCAGCTTATAATG

## **FIGURE 4**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094

><subunit 1 of 1, 379 aa, 0 stop

><MW: 41528, pI: 7.97, NX(S/T): 2

MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK  
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPLL  
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPPGC  
RNGGFCNERRICECPDGFHGHCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST  
TCFNGGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCIGKSKCKCSKGYQGDLCSPVC  
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEEERDP  
PESNYIW

### **Signal peptide:**

amino acids 1-28

### **N-glycosylation site.**

amino acids 88-92, 245-249

### **Casein kinase II phosphorylation site.**

amino acids 319-323

### **Tyrosine kinase phosphorylation site.**

amino acids 370-378

### **N-myristoylation sites.**

amino acids 184-190, 185-191, 189-195, 315-321

### **ATP/GTP-binding site motif A (P-loop).**

amino acids 285-293

### **EGF-like domain cysteine pattern signature.**

amino acids 198-210, 230-242, 262-274, 294-306, 326-338



## FIGURE 5

CGGACGCGTGGGCGTCCGGCGGTTCGACAGCCAGGAGGCGGAGGCGCGCGGGCCAGCCTGGG  
CCCCAGCCCACACCTTCACCAGGGCCCAGGAGCCACC**ATGT**GGCGATGTCCACTGGGGCTAC  
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCAGCAGGGTCGTGGGCGCCGG  
GAGCTAGCACCGGGTCTGCACCTGCGGGGCATCCGGGACGCGGGAGGCCGGTACTGCCAGGA  
GCAGGACCTGTGCTGCCGCGGCCGTGCCGACGACTGTGCCCTGCCCTACCTGGGCGCCATCT  
GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC  
TGCCTCGGCGTGCCACCCCCCTTTTCCCCCGATCCAAGGATGTATGCATGGAGGTCGTATCTA  
TCCAGTCTTGGAACGTACTGGGACAACTGTAACCGTTGCACCTGCCAGGAGAACAGGCAGT  
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG  
GAACCACAGCGCCTTCTGGGGCATGACCCTGGAT**TG**AGGGCATTTCGTACCGCCTGGGCACCA  
TCCGCCCATCTTCTCGGTTCATGAACATGCATGAAATTTATACAGTGCTGAACCCAGGGGAG  
GTGCTTCCCACAGCCTTCGAGGCCTCTGAGAAGTGGCCCAACCTGATTTCATGAGCCTCTTGA  
CCAAGGCAACTGTGCAGGCTCCTGGGCCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT  
CAATCCATTCTCTGGGACACATGACGCCTGTCTGTGCGCCCAGAACCTGCTGTCTTGTGAC  
ACCCACCAGCAGCAGGGCTGCCGCGGTGGGCGTCTCGATGGTGCCTGGTGGTTTCTGCGTCG  
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCC  
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTGCGGGCAAGCGCCAGGCCACTGCC  
CACTGCCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACCTCTGTCTACCGCCT  
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA  
TGGAGGTGCATGAGGACTTCTTCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGC  
CTTGGGAGGCCAGAGAGATAACCGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG  
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGCCAACTCCTGGGGCC  
CAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGCGCGGCGTCAATGAGTGCGACATCGAG  
AGCTTCGTGCTGGGCGTCTGGGGCCGCGTGGGCATGGAGGACATGGGTCATCACTGAGGCTG  
CGGGCACCACGCGGGGTCCGGCCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGCCCAATG  
GGGCGGTGACCCACAGCCTCGCCCCGACAGAGCCCGGGGCGCAGGCGGGCGCCAGGGCGCTAAT  
CCCGGCGCGGGTTCCGCTGACGCAGCGCCCCGCTGGGAGCCGCGGGCAGGCGAGACTGGCG  
GAGCCCCCAGACCTCCAGTGGGGACGGGGCAGGGCCTGGCCTGGGAAGAGCACAGCTGCAG  
ATCCCAGGCCTCTGGCGCCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC  
CCCAATACCCACCCCAATCCCGTATTCTTTTTTTTTTTTTTTTTTTAGACAGGGTCTTGCTCCG  
TTGCCCAGGTTGGAGTGCAGTGGCCCATCAGGGCTCACTGTAACCTCCGACTCCTGGGTTCA  
AGTGACCTCCACCTCAGCCTCTCAAGTAGCTGGGACTACAGGTGCACCACCACACCTGGC  
TAATTTTTGTATTTTTTGTAAAGAGGGGGGTCTCACTGTGTTGCCAGGCTGGTTTCGAAC  
CCTGGGCTCAAGCGGTCCACCTGCCTCCGCTCCCAAAGTGCTGGGATTGCAGGCATGAGCC  
ACTGCACCCAGCCCTGTATTCTTATTCTTCAGATATTTATTTTCTTTTCACTGTTTTAAAA  
TAAAACCAAAGTATTGATAAAAAAAA

## **FIGURE 6**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223

><subunit 1 of 1, 164 aa, 1 stop

><MW: 18359, pI: 7.45, NX(S/T): 1

MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADDC  
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPFPPIQGCMHGGRIYPVLGTYWDNCNR  
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

### **N-glycosylation site.**

amino acids 78-82, 161-165

### **Casein kinase II phosphorylation site.**

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,  
411-415

### **N-myristoylation site.**

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,  
269-275, 378-384, 442-448

### **Amidation site.**

amino acids 26-30, 318-322

### **Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 398-409

## **FIGURE 7**

AGGCTCCTTGGCCCTTTTTCCACAGCAAGCTTNTGCNATCCCGATTTCGTTGTCTCAAATCCA  
ATTCTCTTGGGACACATNACGCCTGTCCTTTNGCCCCAGAACCTGCTGTCTTGTACACCCAC  
CAGCAGCAGGGCTGCCGCGNTGGGCGTCTCGATGGTGCCTGGTGGTTCCTGCGTCGCCGAGG  
GNTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC  
CCCCCTGTATGATGCACAGCCGAGCCATGGGTCTGGGGCAAGCGCCAGGCCACTGCCCACTGC  
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC  
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG  
TGCATGAGGACTTCTTCCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG  
AGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAG

TCCTCTTGGGACACATNACGCCTGTCCTTTNGCCCCAGAACCTGCTGTCTTGTACACCCAC

## FIGURE 8

GCTGCTTGCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT  
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG  
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG  
CAGCTTGAACTGCGTGGATGACTCACAGGACTACTACGTGGGCAAGAAGAACATCACGTGCT  
GTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGCCGGCTGCCGCCATCCTT  
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG  
CCCCGCTGCAGCCCACACTGGGTGTGGTGCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG  
GCCCAGTGGGAGCCTGTCTGGTTCTTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT  
CTGCACCCCTGTCCCCCACCCTGACCCTCCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA  
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCCCTCCAACCCTCTCTGCTGCTGTTTC  
CATGGCCCAGCATTCTCCACCCTTAACCCTGTGCTCAGGCACCTCTTCCCCCAGGAAGCCTT  
CCCTGCCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACCCAGCA  
GGGGACAGGCACTCAGGAGGGCCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA  
GGACAAGAGTCGACGTGAGTTCCTGGGAGTCTCCAGAGATGGGGCCTGGAGGCCTGGAGGAA  
GGGGCCAGGCCTCACATTTCGTGGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT  
AATAAACACCTGTTGGATAAGCCAAAAAA

## **FIGURE 9**

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLLPSSLRCSLHSACCSGDPASYRLWGAPLQPT  
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMVYCTFVPHPDPPMALSRTPTRQISSSDT  
DPPADGPSNPLCCCFHGPAFSTLNPVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

### **Signal peptide:**

amino acids 1-47

### **N-glycosylation site.**

amino acids 31-35, 74-78, 84-88

### **Casein kinase II phosphorylation site.**

amino acids 22-26, 76-80

### **N-myristoylation site.**

amino acids 56-60

### **Amidation site.**

amino acids 70-74

Table 1. Demographic characteristics of the study population	
Age (years)	50.0 ± 10.0
Gender	
Male	50.0%
Female	50.0%
Education (years)	12.0 ± 2.0
Marital status	
Married	80.0%
Single	20.0%
Occupation	
Professional	30.0%
Managerial	20.0%
Technical	10.0%
Skilled	20.0%
Unskilled	20.0%
Income (USD/month)	1000.0 ± 500.0
Health status	
Good	70.0%
Fair	20.0%
Poor	10.0%

CCCACGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCCGCCTGCTGCCCAACCTCACTCTGT  
GCTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGGACCAGGGCGCCATGACC  
GACCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA  
CGTGCAGGTCACCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGGCCAAGC  
TCATAGTGGAGACGGACACGTTTGGCAGCCGGGTTCGCATCAAAGGGGCTGAGAGTGAGAAG  
TACATCTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCCAGCGGGAAGAGCAAAGACTG  
CGTGTTACGGAGATCGTGCTGGAGAACTATAACGGCCTTCCAGAACGCCCGGCACGAGG  
GCTGGTTCATGGCCTTCACGCGGCAGGGGCGGCCCGCCAGGCTTCCCGCAGCCGCCAGAAC  
CAGCGCGAGGCCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCCAACACGC  
CGAGAAGCAGAAGCAGTTCGAGTTTGTGGGCTCCGCCCCCACC CGCCGGACCAAGCGCACAC  
GGCGGCCCCAGCCCCTCACGTAGTCTCTGGGAGGCAGGGGGCAGCAGCCCCTGGGCCGCCTCCC  
CACCCCTTTCCCTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCC  
GAGGGAGGACCCTGAGGGCCGCGAAGCATCCGAGCCCCCAGCTGGGAAGGGGCAGGCCGGTG  
CCCCAGGGGCGGCTGGCACAGTGCCCCCTTCCCGGACGGGTGGCAGGCCCTGGAGAGGAACT  
GAGTGTCACCCTGATCTCAGGCCACCAGCCTCTGCCGGCCTCCCAGCCGGGCTCCTGAAGCC  
CGCTGAAAGGTCAGCGACTGAAGGCCTTGCAAGACAACCGTCTGGAGGTGGCTGTCTCTCAAAA  
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCCCAGCCCCAACTCCTCCTGGCTAGACTGTA  
GGAAGGGACTTTTGTTTGTTTGTTCAGGAAAAAAGAAAGGGAGAGAGAGGAAAAATAG  
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCCAACCCCAACTCCCAGCCC  
CGGAATAAAAACCATTTTTCCTGC

## **FIGURE 11**

MGAARLLPNLTLCQLLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI  
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLGKPSGKSKDCVFTEIVLE  
NNYTAFQONARHEGWFMATRQGRPRQASRSRQNRQEAHFQKRLYQGQLPFPNHAEKQKQFEF  
VGSAPTRRTKRTRRPQPLT

### **Signal peptide:**

amino acids 1-22

### **N-glycosylation site.**

amino acids 9-13, 126-130

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 60-64

### **Casein kinase II phosphorylation site.**

amino acids 65-69

### **Tyrosine kinase phosphorylation site.**

amino acids 39-48, 89-97

### **N-myristoylation site.**

amino acids 69-75, 188-194

### **Amidation site.**

amino acids 58-62

### **HBGF/FGF family signature.**

amino acids 103-128

## FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAG  
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTAC  
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT  
CATTTTGATTTTGCTGTTTATTTTTTTTTTTCTTTTTCTTTTTCCCACCACATTGTATTTTAT  
TTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCAGCCATGGGGCTTTTTTTCCT  
GAAGTCTTGGCTTATCATTTCCCTGGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCTGCC  
CTAGTGTGTGCCGCTGCGACAGGAACTTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG  
CCTCTTGGGATCCCGAGGGCGTAACCGTACTCTACCTCCACAACAACCAAATTAATAATGC  
TGGATTTCTCTGCAGAACTGCACAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC  
AACTGGACGAATTCCTCATGAACCTTCCCAAGAATGTGAGAGTTCTCCATTTGCAGGAAAAAC  
AATATTGAGACCATTTCACGGGCTGCTCTTGCCCAGCTCTTGAAGCTTGAAGAGCTGCACCT  
GGATGACAACCTCCATATCCACAGTGGGGGTGGAAGACGGGGCTTCCGGGAGGCTATTAGCC  
TCAAATTGTTGTTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCTGTGGAC  
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTATATCCGACATGGCCTTCCAGAA  
TCTCACGAGCTTGGAGCGTCTTATTGTGGACGGGAACCTCCTGACCAACAAGGGTATCGCCG  
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTTCAATTGTACGTAATTGCTGTCC  
CACCCTCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTTGCAGGACAACCAGAT  
AAACCACATTCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA  
ACAACCAACTGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACCTGAAGCAGCTC  
ACTGCTCGGAATAACCTTTGGTTTTGTGACTGCAGTATTAAATGGGTACAGAATGGCTCAA  
ATATATCCCTTCATCTCTCAACGTGCGGGGTTTTCATGTGCCAAGGTCTGAACAAGTCCGGG  
GGATGGCCGTCAGGGAATTAAATATGAATCTTTTGTCTGTCCCACCACGACCCCCGGCCTG  
CCTCTCTTCACCCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCCACCCTCTCTAT  
TCCAAACCCTAGCAGAAGCTACACGCCTCCAACTCCTACCACATCGAAACTTCCCACGATTC  
CTGACTGGGATGGCAGAGAAAGAGTGACCCACCTATTTCTGAACGGATCCAGCTCTCTATC  
CATTTTGTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTCTTCACCGTGATGGCATA  
CAAACCTCACATGGGTGAAAATGGGCCACAGTTTAGTAGGGGGCATCGTTCAGGAGCGCATAG  
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT  
TGTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTGTTCAGAGGC  
CACCACCCATGCCTCCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA  
CGTCCCACAGCATGGGCTCCCCCTTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATTT  
GTGCTGGTGGTCTTGCTCAGCGTCTTTTGCTGGCATATGCACAAAAAGGGGCGCTACACCTC  
CCAGAAAGTGGAATACAACCGGGGCCGGCGAAAGATGATTATTGCGAGGCAGGCACCAAGA  
AGGACAACCTCCATCCTGGAGATGACAGAAACAGTTTTTCAGATCGTCTCCTTAAATAACGAT  
CAACTCCTTAAAGGAGATTTTCACTGTCAGCCCATTTACACCCCAAATGGGGGCATTAATTA  
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGC  
ACTGCCATACGTGACAGCCAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAA  
CACACTCGTGTGTGCACATAAAGACACGCAGATTACATTTGATAAATGTTACACAGATGCAT  
TTGTGCATTTGAATACTCTGTAATTTATACGGTGTACTATATAATGGGATTTAAAAAAGTG  
CTATCTTTTCTATTTCAAGTTAATTACAAACAGTTTTGTAACTCTTTGCTTTTTTAAATCTT



## **FIGURE 13**

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP  
EGVTVLVYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTI  
SRAALAQLLKLEELHLDLDDNSISTVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELR  
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD  
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN  
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMAVRELMNLLSCPTTTPGLPLFTP  
APSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLTPTIPDWDGRERVTPPISERIQLSIHFVND  
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL  
DAFNRYAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL  
LSVFCWHMHKKGRYTSQKWKYNRGRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKG  
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 542-561

**N-glycosylation site.**

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

**Casein kinase II phosphorylation site.**

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

**Tyrosine kinase phosphorylation site.**

amino acids 319-328

**N-myristoylation site.**

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,  
522-528, 545-551, 633-639

**Amidation site.**

amino acids 581-585

**Leucine zipper pattern.**

amino acids 164-186

**Phospholipase A2 aspartic acid active site.**

amino acids 39-50

## FIGURE 14

ACTTGGAGCAAGCGGCGGCGGCGGAGACAGAGGCAGAGGCAGAAGCTGGGGCTCCGTCTCGCCTCCACGAGCG  
ATCCCCGAGGAGAGCCGCGGCCCTCGGCGAGGCGAAGAGGCCGACGAGGAAGACCCGGGTGGCTGCGCCCCCTGCC  
TCGCTTCCAGGCGCCGCGGCTGCAGCCTTGCCCCCTTGTCTCGCCTTGAAAATGGAAAAAGATGCTCGCAGGCT  
GCTTTCTGCTGATCCTCGGACAGATCGTCTCTCCCTGCCGAGGCCAGGGAGCGGTACAGTGGGAGGTCCATCT  
CTAGGGGCGAGACACGCTCGGACCCACCCGCGAGACGGCCCTTCTGGAGAGTTCTGTGAGAACAAAGCGGGCAGACC  
TGGTTTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTCATCGTGGACA  
TCTTGCAATTCTTGGACATTGGTCTGATGTCAACCCGAGTGGGCTGCTCCAATATGGCAGCACTGTCAAGAATG  
AGTTCTCCCTCAAGACCTTCAAGAGGAAGTCCGAGGTGGAGCGTGTGTCAAGAGGATGCGGCATCTGTCCACGG  
GCACCATGACTGGGCTGGCCATCCAGTATGCCCTGAACATCGCATTTCTCAGAAGCAGAGGGGGCCCGGCCCTGA  
GGGAGAATGTGCCACGGGTCATAATGATCGTGACAGATGGGAGACCTCAGGACTCCGTGGCCGAGGTGGCTGCTA  
AGGCACGGGACACGGGCATCCTAATCTTTGCCATTGGTGTGGGCCAGGTAGACTTCAACACCTTGAAGTCCATTG  
GGAGTGAGCCCCATGAGGACCATGTCTTCTTGTGGCCAATTTAGCCAGATTGAGACGCTGACCTCCGTGTTCC  
AGAAGAAGTTGTGCACGGCCACATGTGCAGCACCCCTGGAGCATAACTGTGCCCACTTCTGCATCAACATCCCTG  
GCTCATACGCTCTGCAGGTGCAACAAGGCTACATTTCTCAACTCGGATCAGACGACTTGCAGAATCCAGGATCTGT  
GTGCCATGGAGGACCACAACTGTGAGCAGCTCTGTGTGAATGTGCCGGGCTCCTTCGTCTGCGCATGCTACAGTG  
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCCTCAGAAAACCACGGATGTGAAC  
ATGAGTGTGTAAATGCTGATGGCTCTTACCTTTGCCAGTGCCATGAAGGATTTGCTCTTAACCCAGATGAAAAA  
CGTGACAAAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGCCTCAACATGGAGGAGAGCT  
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAAACCTGCAGCCGAGTGGACCACTGTGCAC  
AGCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGGAGGATTCCTTCGTCTGCCAGTGTCTCAGAAGGCTTCC  
TCATCAACGAGGACCTCAAGACCTGCTCCCGGGTGGATTACTGCTGCTGAGTGACCATGGTTGTGAATACTCCT  
GTGTCAACATGGACAGATCCTTTGCCTGTGAGTGTCTGAGGGACACGTGCTCCGAGCGATGGGAAGACGTGTG  
CAAAATTTGACTCTTGTGCTCTGGGGGACCACGGTTGTGAACATTCGTGTGTAAGCAGTGAAGATTCTGTTTGTGT  
GCCAGTGTCTTTGAAGGTTATATACTCCGTGAAGATGGAAAAACCTGCAGAAGGAAGATGTCTGCCAAGCTATAG  
ACCATGGCTGTGAACACATTTGTGTGAACAGTGACGACTCATACAGTGCAGTGTCTGGAGGGATTCCGGCTCG  
CTGAGGATGGGAAACGCTGCCGAAGGAAGGATGTCTGCAAACTCAACCCACCATGGCTGCGAACACATTTGTGTTA  
ATAATGGGAATTCCTACATCTGCAAAATGCTCAGAGGGATTTGTTCTAGCTGAGGACGGAAGACGGTGCAGAAAT  
GCACTGAAGGCCCAATTGACCTGGTCTTTGTGATCGATGGATCCAAGAGTCTTGGAGAAGAGAATTTTGAGGTG  
TGAAGCAGTTTGTCACTGGAATTATAGATTCTTTGACAAATTTCCCCCAAAGCCGCTCGAGTGGGGCTGCTCCAGT  
ATTCACACAGGTCCACACAGAGTTCACTCTGAGAACTTCAACTCAGCCAAAGACATGAAAAAAGCCGTGGCCC  
ACATGAAATACATGGGAAAGGGCTCTATGACTGGGCTGGCCCTGAAACACATGTTTGAGAGAAGTTTTACCCAAG  
GAGAAGGGGCCAGGCCCTTTCCACAAGGGTGGCCAGAGCAGCCATTGTGTTTACCAGCGGACGGGCTCAGGATG  
ACGTCTCCGAGTGGGCCAGTAAAGCCAAGGCCAATGGTATCACTATGTATGCTGTTGGGGTAGGAAAAGCCATTG  
AGGAGGAACACAAAGAGATTGCTCTGAGCCCAACAAAGCATCTCTTCTATGCCGAAGACTTCAGCACAAATGG  
ATGAGATAAGTAAAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG  
CAGGGGAAC TGCCAAAAACGGTCCAACAGCCAACAGAATCTGAGCCAGTCAACATAAATATCCAAGACCTACTTT  
CCTGTTCTAATTTTGAGTGCAACACAGATATCTGTTTGAAGAAGACAATCTTTTACGGTCTACACAAAAGCTTT  
CCCATTCAACAAAACCTTCAGGAAGCCCTTTGGAAGAAAAACACGATCAATGCAAATGTGAAAACCTTATAATGT  
TCCAGAACCCTTGCAACGAAGAAGTAAGAAAAATTAACACAGCGCTTAGAAGAAATGACACAGAGAATGGAAGCCC  
TGGAAAAATCGCCTGAGATACAGATGAAGATTAGAAATCGCGACACATTTGTAGTCATTGTATCACGGATTACAAT  
GAACGCAGTGCAGAGCCCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGTGAAGTAAAACAATCAGTACTGA  
GAAACCTGGTTTGCCACAGAACAAAGACAAGAAGTATACACTAATTTGTATAAATTTATCTAGGAAAAAATCCT  
TCAGAATTTCAAGATGAATTTACCAGGTGAGAATGAATAAGCTATGCAAGGTATTTTGTAAATATACCTGTGGACAC  
AATTTGCTTCTGCCTCATCCTGCCTTAGTGTGCAATCTCATTTGACTATACGATAAAGTTTGCACAGTCTTACTT  
CTGTAGAACACTGGCCATAGGAAATGCTGTTTTTTTGTACTGGACTTTACCTTGATATATGTATATGGATGTATG  
CATAAAATCATAGGACATATGTACTTGTGGAACAAGTTGGATTTTTTTATACAATATTAAATTCACCACTTCAG

## **FIGURE 15**

MEKMLAGCFLILGQIVLLPAEARERSRGRSISRGRHARTHPQTALLESSCENKRADLVFII  
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV  
KMRHLSTGTMGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD  
TGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN  
CAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCQQLCVNVPGSFVCQCYSGYA  
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKPGC  
EHECVNMEESSYYCRCHRGYTLDPNGKTC SRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI  
NEDLKTC SRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSDGKTC AKLDS CALGDHGCE  
HSCVSSSEDSFVCQCFEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLA  
EDGKRCRRKDVCCKSTHHGCEHICVNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLVFVID  
GSKSLGEENFEVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA  
HMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN  
GITMYAVGVGKAIEEELQEIASEPTNKHLEFYAEDFSTMDEISEKLKKGICEALEDSDGRQDS  
PAGELPKTVQQPTESEPVTINIQLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSPLE  
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

### **Signal peptide:**

amino acids 1-23

### **N-glycosylation site.**

amino acids 221-225

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 115-119, 606-610, 892-896

### **Casein kinase II phosphorylation site.**

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,  
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,  
781-785, 819-823, 866-870

### **N-myristoylation site.**

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,  
639-645, 690-696, 752-758, 792-798

### **Amidation site.**

amino acids 314-318, 560-564, 601-605

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,  
540-546, 581-587

## FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTGCGCGAGCCTCG  
GCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGGC  
CATGATTTCCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTTGTTCTTGCGGGCTGA  
GTGCCCTCGCGCCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCCGCAACCGGTTGCAG  
GCGGTGGAGGGAGGGGAAGTGGTGCTTCAGCGTGGTACACCTTGACGGGGAGGTGTCTTC  
ATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC  
AGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC  
ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTA  
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT  
TAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCAT  
GTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA  
GTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCATCCGTG  
GGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC  
AATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC  
AGTGGTTGCTGGAGCTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCC  
TCTTGTAACACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC  
ATTGCTCCCCGGACCTGCCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCTT  
TTCCTCTGTACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCAT  
TGACCCCCACGCCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT  
GGGGCCACCCCTCAACCAATATCCCCCATCCCTGGTGGGGTTTTCTTCTCTGGCTTGAGCCG  
CATGGGTGCTGTGCCTGTGATGGTGCTGCCAGAGTCAAGCTGGCTCTCTGGTATTGATGAC  
CCCACCACTCATTTGGCTAAAGGATTTGGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCAC  
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTC  
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA  
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG  
CTGAAATTAGCTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGC  
CCCCTTGATCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGT  
ATTGATATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTC  
TTATTAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAA  
TGTTTGTATGAAAAA

## **FIGURE 17**

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS  
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPY  
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQCQSPRSKPAVQYQ  
WDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA  
VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWKSSDTISKNGTL  
SSVTSARALRPPHGPPrPGALTPTPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSR  
MGAVPVMVPAQSQAGSLV

### **Signal peptide:**

amino acids 1-29

### **Transmembrane domain:**

amino acids 245-267

### **N-glycosylation site.**

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

### **N-myristoylation site.**

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,  
262-268, 308-314, 363-369, 364-370

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

Figure 1 consists of 11 histograms, labeled (a) through (k), each representing the distribution of the number of non-zero elements in the vector  $x$  for a specific value of  $n$ . The x-axis for all histograms is 'Number of non-zero elements in  $x$ ' with major ticks at 0, 20, 40, 60, 80, and 100. The y-axis is 'Frequency' with major ticks at 0, 20, 40, 60, 80, and 100. The distributions are as follows:

- (a)  $n=1$ : A single bar at 0 with a frequency of 100.
- (b)  $n=2$ : Two bars at 0 and 1. Frequency at 0 is 80, at 1 is 20.
- (c)  $n=3$ : Three bars at 0, 1, and 2. Frequencies are approximately 60, 30, and 10 respectively.
- (d)  $n=4$ : Four bars at 0, 1, 2, and 3. Frequencies are approximately 40, 40, 15, and 5 respectively.
- (e)  $n=5$ : Five bars at 0, 1, 2, 3, and 4. Frequencies are approximately 25, 40, 25, 10, and 5 respectively.
- (f)  $n=6$ : Six bars at 0, 1, 2, 3, 4, and 5. Frequencies are approximately 15, 40, 25, 15, 5, and 5 respectively.
- (g)  $n=7$ : Seven bars at 0, 1, 2, 3, 4, 5, and 6. Frequencies are approximately 10, 40, 25, 20, 10, 5, and 5 respectively.
- (h)  $n=8$ : Eight bars at 0, 1, 2, 3, 4, 5, 6, and 7. Frequencies are approximately 5, 40, 25, 25, 15, 10, 5, and 5 respectively.
- (i)  $n=9$ : Nine bars at 0, 1, 2, 3, 4, 5, 6, 7, and 8. Frequencies are approximately 5, 40, 25, 25, 20, 15, 10, 5, and 5 respectively.
- (j)  $n=10$ : Ten bars at 0, 1, 2, 3, 4, 5, 6, 7, 8, and 9. Frequencies are approximately 5, 40, 25, 25, 20, 15, 10, 10, 5, and 5 respectively.
- (k)  $n=11$ : Eleven bars at 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, and 10. Frequencies are approximately 5, 40, 25, 25, 20, 15, 10, 10, 10, 5, and 5 respectively.

CGCCACCACCTGCGGCCACCGCCAAATGAAACAGCCTCCCGCTCCTAGTGTTTTTTTCCACTTTG  
TTGAATTGTTTCTATACTCAAAATTGACCAAGACACCTTGTCTCCCAAATGCAAAATGTGA  
AATACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTTTCAGGAAATGGTGTCACAA  
TTTGTGAAGATGATAATGAATGTGGAAATTTAACTCAGTCCTGTGGCGAAAAATGCTAATTGC  
ACTAACACAGAAGGAAGTTATTATTGTATGTGTGTACCTGGCTTCAGATCCAGCAGTAACCA  
AGACAGGTTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACTGCCATT  
TAGATAATGTCTGTATAGCTGCAAATATTAATAAAACTTTAACAAAAATCAGATCCATAAAA  
GAACCTGTGGCTTTGCTACAAGAAGTCTATAGAAATTCGTGTGACAGATCTTTCACCAACAG  
TATAATTACATATATAGAAATATTAGCTGAATCATCTTCATTACTAGGTTACAAGAACAACA  
CTATCTCAGCCAAGGACACCCTTTCTAACTCAACTCTTACTGAATTTGTAAAAACCGTGAAT  
AATTTTGTTCAAAGGGATACATTTTGTAGTTTGGGACAAGTTATCTGTGAATCATAGGAGAAC  
ACATCTTACAAAACCTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCAGAGCTTCC  
AAAAGACCACAGAGTTTGATACAAATTCAACGGATATAGCTCTCAAAGTTTTCTTTTTTGAT  
TCATATAACATGAAACATATTTCATCCTCATATGAATATGGATGGAGACTACATAAATATATT  
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGTTGCATTTTTTATATTATA  
AGAGTATTGGTCTTTTGCTTTTCATCATCTGACAACCTTCTTATTGAAACCTCAAATTATGAT  
AATTCGAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTTCAGTCTCAATGAGCTCAAACCC  
ACCCACATTATATGAACTTGAAAAAATAACATTTACATTAAGTTCATCGAAAGGTCACAGATA  
GGTATAGGAGTCTATGTGCATTTTGAATTACTCACCTGATACCATGAATGGCAGCTGGTCT  
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT  
GACACATTTTGCAATTTTGATGTCTCTGGTCTTCCATTGGTATTAAAGATTATAATATTC  
TTACAAGGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTGCCATATGCATTTTT  
ACCTTCTGGTTCTTCAGTGAAATTCAAAGCACCAGGACAACAATTCACAAAAATCTTTGCTG  
TAGCCTATTTCTTGCTGAACTTGTTTTTCTTGTTGGGATCAATACAAATACTAATAAGCTCT  
TCTGTTCAATCATTTGCCGACTGCTACACTACTTCTTTTTAGCTGCTTTTGCATGGATGTGC  
ATTGAAGGCATACATCTCTATCTCATTTGTTGTGGGTGTCATCTACAACAAGGGATTTTTTGCA  
CAAGAATTTTTATATCTTTGGCTATCTAAGCCCAGCCGTGGTAGTTGGATTTTTCGGCAGCAC  
TAGGATACAGATATTATGGCACAACCAAAGTATGTTGGCTTAGCACCGAAAACAACTTTAT  
TGGAGTTTTATAGGACCAGCATGCCTAATCATTCTTGTTAATCTCTTGGCTTTTGGAGTCAT  
CATATACAAAGTTTTTCTGCACACTGCAGGGTTGAAACCAGAAGTTAGTTGCTTTGAGAACA  
TAAGGTCTTGTGCAAGAGGAGCCCTCGCTCTTCTGTTCTTCTCGGCACCACCTGGATCTTT  
GGGGTTCTCCATGTTGTGCACGCATCAGTGGTTACAGCTTACCTCTTCACAGTCAGCAATGC  
TTTCCAGGGGATGTTCATTTTTTTTATTCTCTGTGTGTTTTATCTAGAAAGATTCAAGAAGAAT  
ATTACAGATTGTTCAAAAATGTCCCCTGTTGTTTTGGATGTTTAAGGTAAACATAGAGAATG  
GTGGATAATTACAACCTGCACAAAAATAAAAAATTCCAAGCTGTGGATGACCAATGTATAAAAA  
TGACTCATCAAATTATCCAATTATTAACCTACTAGACAAAAAGTATTTTTAAATCAGTTTTTCT  
GTTTATGCTATAGGAACTGTAGATAATAAGGTAAAAATTATGTATCATATAGATATACTATGT  
TTTTCTATGTGAAATAGTTCTGTCAAAAATAGTATTGCAGATATTTGGAAAGTAATTGGTTT  
CTCAGGAGTGATATCACTGCACCCAAGGAAAGATTTTCTTTCTAACACGAGAAGTATATGAA  
TGTCCTGAAGGAAACCACTGGCTTGATATTTCTGTGACTCGTGTTGCCTTTGAAACTAGTCC  
CCTACCACCTCGGTAATGAGCTCCATTACAGAAAGTGGAACATAAGAGAATGAAGGGGCAGA  
ATATCAAAACAGTGAAAAGGGAATGATAAGATGTATTTTGAATGAACTGTTTTTTCTGTAGAC  
TAGCTGAGAAATTGTTGACATAAAAATAAAGAATTGAAGAAACACATTTTACCATTTTGTGAA  
TTGTTCTGAACTTAAATGTCCACTAAAACAACCTTAGACTTCTGTTTGCTAAATCTGTTTCTT  
TTTCTAATATTCTAAAAAAGGTTTACCTCCACAAATTGAAAAAAGGTTTACCTCCACAAATGAAAAA  
AAAAAAGGTTTACCTCCACAAATTGAAAAAAGGTTTACCTCCACAAATTGAAAAAAGGTTTACCTCCACAAATGAAAAA

## **FIGURE 19**

MKRLPLLVVVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC  
GNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIENTVNANCHLDNVCIAA  
NINKTLTKIRSIKEPVALLOEVYRNSVTDLSPTDIITYIEILAESSSLLGYKNNTISAKDTL  
SNSTLTETVKTNNFVQRDTFVVWDKLSVNHRRTHLTKLMHTVEQATLRISQSFQKTTEFDT  
NSTDIALKVFFFDSDYNMKHIHPHMNMDGDYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS  
SSDNFLLKPQNYDNSEEEERVISVISVSMSSNPPTLYELEKITFTLSHRKVTDTRYSLCAF  
WNYSPTMNGSWSSEGCELTYSNETHTSCRCNHLTHFAILMSSGPSIGIKDYNILTRITQLG  
IIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCIIAGL  
LHYFFLAFAWMCIEGHIHLYLJVGVYINKGFLHKNFYIFGYLSPAVVVGFSALGYRYYGT  
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA  
LALLFLLGTTWIFGVLVHVVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEYYRLFKNV  
PCCFGCLR

### **Signal peptide:**

amino acids 1-19

### **Transmembrane domain:**

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,  
648-664

### **N-glycosylation site.**

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,  
188-192, 249-253, 381-385, 395-399

### **Glycosaminoglycan attachment site.**

amino acids 49-53

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 360-364

### **Casein kinase II phosphorylation site.**

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,  
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,  
346-350, 608-612

### **Tyrosine kinase phosphorylation site.**

amino acids 36-44, 669-677, 670-678

### **N-myristoylation site.**

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,  
434-440, 480-486, 521-527

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 75-87

## **FIGURE 20**

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTTCCAAAGNG  
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTTATATTATAAGAGTAT  
TGGTCCCTTTGCTTTCATCATCTGACAACTTCTTATTGAAACCTCAAAATTATGATAATTCT  
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTTCAGTCTCAATGAGCTCAAACCCACCCAC  
ATTATATGAACTTGAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATAGGTATA  
GGAGTCTATGTGGCATTTTGGAAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG  
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA  
TTTTGCAATTTTGATGTCCTCTGGTCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA  
GGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTGCCATATGCATTTTTACCTTC  
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA

TCCTGAGGAGG



## FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGGCCG  
CTAAGCGAGGCCTCCTCCTCCCGCAGATCCGAACGGCCTGGGCGGGGTACCCCCGGCTGGGA  
CAAGAAGCCGCGCCTGCCTGCCCGGGCGGGGAGGGGGCTGGGGCTGGGGCCGGAGGCGG  
GGTGTGAGTGGGTGTGTGCGGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG  
TGTCTTGGGCACCTACCCGTGGGGGCCCGTAAGGCGCTACTATATAAGGCTGCCGGCCCCGGAG  
CCGCCGCGCCGTCAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC  
GGCACTCACAGCCCCGAGCGCATCCCGGTGCGCGCCAGCCTCCCGCACCCCCATCGCCGG  
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGGTCCACGTATGG  
ATCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGGCGCCCCCTCGCCTTCTCGGACGCGGGGCC  
CCACGTGCACTACGGCTGGGGCGACCCCATCCGCCTGCGGCACCTGTACACCTCCGGCCCCC  
ACGGGCTCTCCAGCTGCTTCTGCGCATCCGTGCCGACGGCGTCTGTGACTGCGCGCGGGGC  
CAGAGCGCGCACAGTTTGCTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGG  
CGTGACACAGCGTGCGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGT  
ACTCGGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCCAGATGGCTACAATGTGTACCGA  
TCCGAGAAGCACCGCCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA  
CAGAGGCTTTTCTTCCACTCTCTCATTTCTGCCCATGCTGCCCATGGTCCCAGAGGAGCCTG  
AGGACCTCAGGGGCCACTTGGAATCTGACATGTTCTCTTCGCCCCCTGGAGACCGACAGCATG  
GACCCATTTGGGCTTGTACCCGACTGGAGGCCGTGAGGAGTCCAGCTTTGAGAAGTAACT  
GAGACCATGCCCCGGCCTCTTCACTGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGGACG  
TGCTTCTACAAGAACAGTCCTGAGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAA  
GTTGTACATATTAGAGTTTTTCCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGAT  
CATAACATTGTAAGCCTGTAGCTTGCCCAGCTGCTGCCTGGGCCCCCATTCTGCTCCCTCGA  
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAAC  
TCACTTCTTTTGAAAAATTCCTATGTCAAGCTGAAATTCTCTAATTTTTTCTCATCACTTC  
CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTTTAATTTAGGAACAGGTGATCCACTCTGTA  
AAACAGCAGGTAAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG  
ACCATTTGCCCTTCCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGCCCACCAG  
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACTTGAGAATTCCCC  
CTGAGGCCAGTTCTGTGTCATGGATGCTGTCTGAGAATAACTTGCTGTCCCGGTGTACCTGC  
TTCCATCTCCCAGCCCACCAGCCCTCTGCCCACCTCACATGCCTCCCCATGGATTGGGGCCT  
CCCAGGCCCCCACCTTATGTCAACCTGCACTTCTTGTTCAAAAATCAGGAAAAGAAAAGAT  
TTGAAGACCCCAAGTCTTGTCATAAATCTGCTGTGTGGAAGCAGCGGGGAAGACCTAGAAC  
CCTTTCCCCAGCACTTGTTTTTCCAACATGATATTTATGAGTAATTTATTTTGTATATGTACA  
TCTCTTATTTTCTTACATTATTTATGCCCCCAAATTATATTTATGTATGTAAGTGAGGTTTG  
TTTTGTATATTAAATGGAGTTTGTGTGT

## **FIGURE 22**

MRSGCVVHVWILAGLWLA VAGRPLAFSDAGPHVHYGWGDP IRLRHLYTSGPHGLSSCFLRI  
RADGVVDCARGQSAHSLLEIKAV ALRTVAIKGVH SVRYLCMGADGKMQGLLQYSEEDCAFEE  
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD  
MFSSPLETDSMDPFGLVTGLEAVRSPSF EK

### **Signal peptide:**

amino acids 1-22

### **Casein kinase II phosphorylation site.**

amino acids 78-82, 116-120, 190-194, 204-208

### **N-myristoylation site.**

amino acids 15-21, 54-60, 66-72, 201-207

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 48-59

## FIGURE 23

CCCAGAAGTTCAAGGGCCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCTCGACCTCCTCA  
GAGCAGCCGGCTGCCGCCCCGGGAAGATGGCGAGGAGGAGCCGCCACCGCCTCCTCCTGCTG  
CTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTTCTGCCCCAAA  
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAAAACCCCAA  
AGAAGACTGTTTCCTCCAGATTAGAGTGGAAGAACTGGGTCGGAGTGTCTCCTTTGTCTAC  
TATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCG  
GATCAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG  
AGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT  
CCATCATGTGAAGTACCTCTTCTGCTCTGAGTGGAAGTGTGGTAGAGCTACGATGTCAAGA  
CAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAGGATGGCATCCGTTTGCTAGAAA  
ATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATAACAAATGAATACAAAACTGGAAGT  
CTGCAATTTAATACTGTTTCCAACTGGACACTGGAGAATATTCCTGTGAAGCCCGCAATTC  
TGTTGGATATCGCAGGTGTCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA  
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTTCCGTTTGTGGCCTTGGTGTATGCTAT  
GCTCAGAGGAAAGGCTACTTTTCAAAGAAACCTCCTTCCAGAAGAGTAATTCTTCATCTAA  
AGCCACGACAATGAGTGAAAATGTGCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGAAGG  
CCGCGGCGGGCGGATCACGAGGTGAGGAGTTCTAGACCAGTCTGGCCAATATGGTGAAACCC  
CATCTCTACTAAAATACAAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTTCAGCTGC  
TTGGGAGACAGGAGAATCACTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC  
CACTGCAGTCCAGCCTGGGTAACAGAGCAAGATTCCATCTCAAAAAATAAAATAAATAAATA  
AATAAATACTGGTTTTTTACCTGTAGAATTCTTACAATAAATATAGCTTGATATTC

## **FIGURE 24**

MARRSRHRLLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLE  
WKKLGRSVSFVYYQQTQLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQNLEED  
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQST  
NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNVSGYRRCPGKRMQVDDLNISGIIAAVVVVA  
LVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWCAAAGGSRGQEF

### **Signal peptide:**

amino acids 1-20

### **Transmembrane domain:**

amino acids 130-144, 238-258

### **N-glycosylation site.**

amino acids 98-102, 187-191, 236-240, 277-281

### **Casein kinase II phosphorylation site.**

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

### **N-myristoylation site.**

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

### **Amidation site.**

amino acids 226-230

FOR "9564060"

## FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAACTGCTTTTCAAGACGAGGAAGAGGAGGAGAAAGAG  
AAAGAAGAGGAAGATGTTGGGCAACATTTATTTAACATGCTCCACAGCCCGGACCCTGGCAT  
CATGCTGCTATTCTTGCAAATACTGAAGAAGCATGGGATTTAAATATTTTACTTCTAAATAA  
ATGAATTACTCAATCTCCTATGACCATCTATACATACTCCACCTTCAAAAAGTACATCAATA  
TTATATCATTAAGGAAATAGTAACCTTCTCTTCTCCAATATGCATGACATTTTTTGGACAATG  
CAATTGTGGCACTGGCACTTATTTTACGTGAAGAAAACTTTGTGGTTCTATGGCATTTCATCA  
TTTGACAAATGCAAGCATCTTCTTATCAATCAGCTCCTATTGAACTTACTAGCACTGACTG  
TGGAATCCTTAAGGGCCCATACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT  
CCGAATTCATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG  
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTTGGTTTACACCCAGATCCATTTAT  
ATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCTTTTAACTTTCCAGCCAGATTGCC  
AGCTAACACACAGATTCTTCTCCTACAGACTAACAAATATTGCAAAAATTGAATACTCCACAG  
ACTTTCCAGTAAACCTTACTGGCCTGGATTTATCTCAAAACAATTTATCTTCAGTCACCAAT  
ATTAATGTAAAAAGATGCCTCAGCTCCTTTCTGTGTACCTAGAGGAAAACAACTTACTGA  
ACTGCCTGAAAAATGTCTGTCCGAACCTGAGCAACTTACAAGAACTCTATATTAATCACAAC  
TGCTTTCTACAATTTACCTGGAGCCTTTATTGGCCTACATAATCTTCTTCGACTTCATCTC  
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTTGATGCTCTTCCAAATCTAGAGAT  
TCTGATGATTGGGGAAAATCCAATTATCAGAATCAAAGACATGAACTTTAAGCCTCTTATCA  
ATCTTCGCAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCTTGGTT  
GGACTGGAAAACCTTAGAAAGCATCTCTTTTTTACGATAACAGGCTTATTAAAGTACCCCATGT  
TGCTCTTCAAAAAGTTGTAAATCTCAAATTTTTTGGATCTAAATAAAAATCCTATTAATAGAA  
TACGAAGGGGTGATTTTAGCAATATGCTACACTTAAAAGAGTTGGGGATAAATAATATGCCT  
GAGCTGATTTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTTAAGAAAAATAGAAGC  
TACTAACAAACCCTAGATTGTCTTACATTACCCCCAATGCATTTTTTCAGACTCCCCAAGCTGG  
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCATTGAGTCTCTG  
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCCATCAGGTGTGACTGTGTGCATCCGTTG  
GATGAACATGAACAAAACCAACATTTCGATTTCATGGAGCCAGATTCACTGTTTTGCGTGGACC  
CACCTGAATTCGAAGTCAAGATGTTTCGGCAAGTGCATTTTCAGGGACATGATGGAAATTTGT  
CTCCCTCTTATAGCTCCTGAGAGCTTTCTTCTAATCTAAATGTAGAAGCTGGGAGCTATGT  
TTCTTTTCACTGTAGAGCTACTGCAGAACCACAGCCTGAAATCTACTGGATAACACCTTCTG  
GTCAAAAACCTCTTGCTAATACCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAACACTA  
GATATAAATGGCGTAACTCCCAAAGAAGGGGGTTTATATACTTGTATAGCAACTAACCTAGT  
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTTTCCACAAGATAACAATG  
GCTCTTTGAATATTAAAATAAGAGATATTCAGGCCAATTCAGTTTTTGGTGTCTCTGGAAAGCA  
AGTTCTAAAATTCTCAAATCTAGTGTAAATGGACAGCCTTTGTCAAGACTGAAAATTCTCA  
TGCTGCGCAAAGTGCTCGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC  
CATCAACTGAGTATAAAATTTGTATTGATATTCCACCATCTATCAGAAAAACAGAAAAAAA  
TGTGTAAATGTCACCACCAAAGGTTTGCACCCTGATCAAAAAGAGTATGAAAAGAATAATAC  
CACAACACTTATGGCCTGTCTTGGAGGCCTTCTGGGGATTATTGGTGTGATATGTCTTATCA  
GCTGCCTCTCTCCAGAAATGAACTGTGATGGTGGACACAGCTATGTGAGGAATTACTTACAG  
AAACCAACCTTTGCATTAGGTGAGCTTTATCCTCCTCTGATAAATCTCTGGGAAGCAGGAAA  
AGAAAAAAGTACATCACTGAAAGTAAAAGCAACTGTTATAGGTTTACCAACAAATATGTCCT  
AAAAACCACCAAGGAAACCTACTCCAAAAATGAAC

## **FIGURE 26**

MKDMPLRIHVLLGLAITTLVQAVDKKVDPCRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT  
FPARLPANTQIILLQTNNAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE  
ENKLTPEKCLSELNLQELYINHNLSTISPGAFIHLNLLRLHLNSNRLQMINSKWFDA  
LPNLEILMIGENPIIRIKDMNFKPLINLRSVLVIAGINLTEIPDNALVGLENLESISFYDNRL  
IKVPHVALQKVVNLFKFLDLNKNPINRIRRGDFSNNMLHLKELGINNMPELISIDSLAVDNLPD  
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSALYHGTIESLPNLKEISIHSPNIRC  
DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGNVRQVHFRDMMEICLPLIAPESFPSNLNV  
EAGSYVSFHCRTAEAPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLDINGVTPKEGGLYTC  
IATNLVGADLKSVMIKVDGSPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFFV  
KTENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE  
YEKNNTTTLMACLGGLLGIIGVICLISCLSPENMCDGGHSYVRNYLQKPTFALGELYPPPLIN  
LWEAGKEKSTSLKVKATVIGLPTNMS

### **Signal sequence:**

amino acids 1-22

### **Transmembrane domain:**

amino acids 633-650

### **N-glycosylation site.**

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,  
608-612, 624-628, 625-629

### **Casein kinase II phosphorylation site.**

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

### **Tyrosine kinase phosphorylation site.**

amino acids 570-579

### **N-myristoylation site.**

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,  
491-497, 492-498, 634-640, 702-708

### **Cell attachment sequence.**

amino acids 277-280

## FIGURE 27

GCCCCGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG  
CTGCAGCCTTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC  
CACGCTTGTTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCCAGCATGAATCT  
GGTAGACCTGTGGTTAACCCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTTTGTTCTTA  
TGATACTGTGCTTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCCTCTGGG  
GGTTTAAATGTACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCCTCCTGA  
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTTAAGG  
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAAATGGCATTGAGTTTATCGATGAGCAT  
GCCTTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG  
TGTGCACAAAAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAACCCCTGGC  
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCAC  
AACGTGATCTGTAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC  
CAACGACGCTGACCTTTGTAACCTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCA  
TGTTTGGCTGGTTCACTATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAG  
GATGCCCCGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA  
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAACTGACTGTCATTGAGAAAGAAAGAAA  
GTAGTTTGCGATTGCAGTAGAAATAAGTGGTTTACTTCTCCCATCCATTGTAAACATTTGAA  
ACTTTGTATTTTCAAGTTTTTTTTTGAATTATGCCACTGCTGAACTTTTAACAAACACTACAACA  
TAAATAATTTGAGTTTAGGTGATCCACCCCTTAATTGTACCCCGATGGTATATTTCTGAGT  
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTT  
AATTTAAAAGCAAATAAAAGCTTAACCTTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAACA

## **FIGURE 28**

MNLVDLWLTRSLMCLLLQSFVLMILCFHSASMCPKGCLCSSSGGLNVTCSNANLKEIPRDL  
PPETVLLYLDSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDSLSDNR  
IQSVHKNAFNNLKARARIANNPWHCCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPFL  
NAANDADLCNLPKKTDDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLSRQKK  
ADEPDDISTVV

### **Signal sequence:**

amino acids 1-33

### **Transmembrane domain:**

amino acids 205-220

### **N-glycosylation site.**

amino acids 47-51, 94-98

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 199-203

### **Casein kinase II phosphorylation site.**

amino acids 162-166, 175-179

### **N-myristoylation site.**

amino acids 37-43, 45-51, 110-116



## FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGCGCCCGAGATGCAGGTGAGCAAGAGGATGCTGGCGGGG  
GGCGTGAGGAGCATGCCCAGCCCCCTCCTGGCCTGCTGGCAGCCCATCCTCCTGCTGGTGCT  
GGGCTCAGTGCTGTCAGGCTCGGCCACGGGCTGCCCGCCCGCTGCGAGTGCTCCGCCCAGG  
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAGTCCCCGAGGGCATCCCCACCGAG  
ACGCGCCTGCTGGACCTAGGCAAGAACCGCATCAAAACGCTCAACCAGGACGAGTTCGCCAG  
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGCCCGGCG  
CCTTCAACAACCTCTTCAACCTCCGGACGCTGGGTCTCCGAGCAACCGCCTGAAGCTCATC  
CCGCTAGGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAAGAT  
CGTTATCCTACTGGACTACATGTTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG  
ACAATGACCTCGTCTACATCTCTCACCGCGCCTTCAGCGGCCTCAACAGCCTGGAGCAGCTG  
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCCACCTGCACGGCCT  
CATCGTCCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGC  
TGTACCGACTCAAGGTCTTGAGATCTCCCACTGGCCCTACTTGACACCATGACACCCAAC  
TGCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC  
CTACCTGGCCGTCCGCCACCTAGTCTATCTCCGCTTCTCAACCTCTCCTACAACCCCATCA  
GCACCATGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGC  
GGGCAGCTGGCCGTGGTGGAGCCCTATGCCTTCCGCGGCCTCAACTACCTGCGCGTGCTCAA  
TGTCTCTGGCAACCAGCTGACCACACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGG  
AGACACTCATCTGGACTCCAACCCGCTGGCCTGCGACTGTCGGCTCCTGTGGGTGTTCCGG  
CGCCGCTGGCGGCTCAACTTCAACCGGCAGCAGCCACGTGCGCCACGCCCAGTTTGTCCA  
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCCACTACTTCACCTGCCGCCGCG  
CCCGCATCCGGGACCGCAAGGCCCAGCAGGTGTTTGTGGACGAGGGCCACACGGTGCAGTTT  
GTGTGCCGGGCCGATGGCGACCCGCCGCCCATCCTCTGGCTCTCACCCCGAAAGCACCT  
GGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCT  
ACGCCCAGGTACAGGACAACGGCACGTACCTGTGCATCGCGGCCAACGCGGGCGGCAACGAC  
TCCATGCCCCGCCACCTGCATGTGCGCAGCTACTCGCCCGACTGGCCCCATCAGCCCAACAA  
GACCTTTCGCTTTTCATCTCCAACCAGCCGGGCGAGGGAGAGGCCAACAGCACCCGCGCCACTG  
TGCTTTTCCCTTTCGACATCAAGACCCTCATCATCGCCACCACCATGGGCTTCATCTCTTTC  
CTGGGCGTCTCCTCTTCTGCCTGGTGTGCTGCTGTTTCTCTGGAGCCGGGGCAAGGGCAACAC  
AAAGCACAACATCGAGATCGAGTATGTGCCCCGAAAGTCGGACGCAGGCATCAGCTCCGCCG  
ACGCGCCCCGCAAGTTCAACATGAAGATGATA**TGAG**AGCCGGGGCGGGGGCAGGGACCCCCG  
GGCGGCCGGGCAGGGGAAGGGGCCTGGTGCACCTGCTCACTCTCCAGTCTTCCCACCTC  
CTCCCTACCTTCTACACACGTTCTCTTCTCCCTCCCGCCTCCGTCCCCTGCTGCCCCCG  
CCAGCCCTCACCACCTGCCCTCCTTCTACCAGGACCTCAGAAGCCCAGACCTGGGGACCCCA  
CCTACACAGGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCGGCAGAGTCA  
ATAATTCAATAAAAAAGTTACGAACCTTCTCTGTAACCTTGGGTTTCAATAATTATGGATTTT  
TATGAAAACCTTGAAATAATAAAAAGAGAAAAAACTAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 30**

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSLSGSATGCPPRCECSAQDRAVLCHRKCF  
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEEELELNENIVSAVEPGAFFNNLFNLRTL  
GLRSNRLKLIPLGVFTGLSNLTKQDISENKIVILLDYMFDLYNLKSLEVGDNDLVYISHRA  
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVLEISH  
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMLHEL  
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTLEESVFHSGVGNLETLILDSNPLA  
CDCRLLWVFRRRWRLNFNRRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV  
FVDEGHTVQFVCRADGDPFPAILWLSPRKHLVSAKSNRGLTVFPDGTLEVRYAQVQDNGTYL  
CIAANAGGNDSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI  
IATTMGFISFLGVVLFCLVLLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

### **Signal sequence:**

amino acids 1-41

### **Transmembrane domain:**

amino acids 556-578

### **N-glycosylation site.**

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,  
492-496, 505-509, 526-530, 542-546

### **Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,  
607-611

### **Tyrosine kinase phosphorylation site.**

amino acids 590-598

### **N-myristoylation site.**

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,  
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

## FIGURE 31

CCCACGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTTCGGTCAAC  
ATCGTAGTCCACCCCTCCCCATCCCCAGCCCCGGGGATTAGGCTCGCCAGCGCCAGCC  
AGGGAGCCGGCCGGGAAGCGCGATGGGGGCCCCAGCCGCCTCGCTCCTGCTCCTGCTCCTGC  
TGTTGCCTGCTGCTGGGCGCCCGGCGGGGCCAACCTCTCCAGGACGACAGCCAGCCCTGG  
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTGCTCAAGTGCCAAGTGAAAGATCA  
CGAGGACTCATCCCTGCAATGGTCTAACCCCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGA  
GAGCCCTTCGAGATAATCGAATTCAGCTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGC  
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGT  
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCACAGAAGCCCATCATCACTGGTT  
ATAAATCTTCATTACGGGAAAAAGACACAGCCACCCTAACTGTCAGTCTTCTGGGAGCAAG  
CCTGCAGCCCGGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCAT  
ACAGGAAGATCCCAATGGTAAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCC  
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC  
AGATCCACCTCTCAACGCATTGAAGTTTTATACACACCAACTGCGATGATTAGGCCAGACCC  
TCCCCATCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCC  
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT  
GCCCTGATCTTCCCTTTCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG  
CAACATGGGCAGCTACAAGGCCTACTACACCCTCAATGTTAATGACCCCAGTCCGGTGCCCT  
CCTCCTCCAGCACCTACCACGCCATCATCGGTGGGATCGTGGCTTTCATTGTCTTCTGCTG  
CTCATCATGCTCATCTTCTTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA  
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG  
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTTTCATCTAGAGGCGCCTGCCCACTTCTGCTG  
GCCCCCAGGGGCCCTGTGGGGACTGCTGGGGCCGTACCAACCCGGACTTGTACAGAGCAA  
CCGCAGGGCCGCCCTCCCGCTTGCTCCCCAGCCCACCCACCCCTGTACAGAATGTCTGC  
TTTGGGTGCGGTTTTGTACTCGGTTTGGAATGGGGAGGGAGGGCGGGGGGAGGGGAGGG  
TTGCCCTCAGCCCTTCCGTGGCTTCTCTGCATTTGGGTTATTATTATTTTGTAAACAATCC  
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACA  
AACAAAAACA

## **FIGURE 32**

MGAPAASLLLLLLLLFACWAPGGANLSQDDSQPWTSDETVVAGGTVVVLKCQVKDHEDSSLQW  
SNPAQQTLTYFGEKRALRDNRILVTSTPHELSSISISNVALADEGEYTCSTFTMPVRTAKSLV  
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK  
TFTVSSSVTFQVTRREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ  
KLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA  
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLI FLGHYLIRHKGYLT THEAKGSDD  
APDADTAIINAEGGQSGGDDKKEYFI

### **Signal sequence:**

amino acids 1-20

### **Transmembrane domain:**

amino acids 331-352

### **N-glycosylation site.**

amino acids 25-29, 290-294

### **Casein kinase II phosphorylation site.**

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

### **N-myristoylation site.**

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,  
306-310, 334-340, 360-364, 385-389, 386-390

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCTTTTCTTCTCCTTTCCTGG  
CTTCGGACATTGGAGCACTAAATGAACTTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTG  
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTTAAAAATGCTGCTTTGGATTCTGTT  
GCTGGAGACGTCTCTTTGTTTTGCCGCTGGAAACGTTACAGGGGACGTTTGCAAAGAGAAGA  
TCTGTTCCCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAGGGCTTCACA  
AGTCTGCAGCGTTTCACTGCCCCGACTTCCCAGTTTTTACCATTTATTTCTGCATGGCAATTC  
CCTCACTCGACTTTTCCCTAATGAGTTCGCTAACTTTTATAATGCGGTTAGTTTGCACATGG  
AAAACAATGGCTTGCATGAAATCGTTCCGGGGGCTTTTCTGGGGCTGCAGCTGGTGAAAAGG  
CTGCACATCAACAACAACAAGATCAAGTCTTTTCGAAAGCAGACTTTTCTGGGGCTGGACGA  
TCTGGAATATCTCCAGGCTGATTTTAAATTTATTACGAGATATAGACCCGGGGGCTTCCAGG  
ACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCTTACCTGCCAAC  
GTGTTCCAGTATGTGCCCATCACCCACCTCGACCTCCGGGGTAACAGGCTGAAAACGCTGCC  
CTATGAGGAGGTCTTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCTT  
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTCCCAAGAATGCC  
CTGATCGGCCGAGTGGTCTGCGAAGCCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC  
CACCGAACAGGACTTGTGTCTTTGAAAAACCGAGTGGATTCTAGTCTCCCGCGCCCCCTG  
CCCAAGAAGAGACCTTTGCTCCTGGACCCCTGCCAACTCCTTTCAAGACAAATGGGCAAGAG  
GATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCAGGCAACTGGCAGAT  
CAAAATCAGACCCACAGCAGCGATAGCGACGGGTAGCTCCAGGAACAAACCTTAGCTAACA  
GTTTACCCTGCCCTGGGGGCTGCAGCTGCGACCACATCCAGGGTTCGGGTTTAAAGATGAAC  
TGCAACAACAGGAACGTGAGCAGCTTGGCTGATTTGAAGCCCAAGCTCTCTAACGTGCAGGA  
GCTTTTCTTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTTTGTGGATTACAAGA  
ACCTCATTTCTGTTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACAACACTTTCAAG  
AACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCGGGA  
GAAATTCGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA  
TCCTCCCGGGCACCTTTCAATGCCATGCCCAAACCTGAGGATCCTCATTCTCAACAACAACCTG  
CTGAGGTCCCTGCCTGTGGACGTGTTTCGCTGGGGTCTCGCTCTCTAAACTCAGCCTGCACAA  
CAATTACTTTCATGTACCTCCCGGTGGCAGGGGTGCTGGACCAGTTAACCTCCATCATCCAGA  
TAGACCTCCACGGAACCCCTGGGAGTGCTCCTGCACAATTGTGCCTTTCAAGCAGTGGGCA  
GAACGCTTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTTCTT  
TAGAAAGGATTTTCATGCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT  
CGCCACGTTAACTTCGCACAGTAAAAACAGCACTGGGTTTGGCGGAGACCGGGACGCACTCC  
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTTGGTCCCGGGACTGCTGCTGGT  
GTTTGTACCTCCGCCTTACCGTGGTGGGCATGCTCGTGTTTATCCTGAGGAACCGAAAGC  
GGTCCAAGAGACGAGATGCCAACTCCTCCGCGTCCGAGATTAATTCCCTACAGACAGTCTGT  
GACTCTTCCTACTGGCACAATGGGCCTTACAACGCAGATGGGGCCACAGAGTGTATGACTG  
TGGCTCTCACTCGCTCTCAGACTAAGACCCCCAACCCCAATAGGGGAGGGCAGAGGGAAGGCG  
ATACATCCTTCCCCACCGCAGGCACCCCGGGGGCTGGAGGGGCGTGTACCCAAATCCCCGCG  
CCATCAGCCTGGATGGGCATAAGTAGATAAAATAACTGTGAGCTCGCACAAACCGAAAGGGCCT  
GACCCCTTACTTAGCTCCCTCCTTGAACAAGAGCAGACTGTGGAGAGCTGGGAGAGCGCA  
GCCAGCTCGCTCTTTGCTGAGAGCCCCCTTTTGACAGAAAGCCCAGCACGACCTGCTGGAAG  
AACTGACAGTGCCCTCGCCCTCGGCCCGGGGCTGTGGGGTTGGATGCCGCGGTTCTATAC  
ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTTTCCCTGTGGATTAG  
CCCCGTGATGGCTCCCTGTTGGCTACGCAGGGATGGGCAGTTGCACGAAGGCATGAATGTAT  
TGTAATAAGTAACTTTGACTTCTGAC

## **FIGURE 34**

MLLWILLLETSLCFAAGNVTGDVCKEIKCSCNEIEGDLHVDCEKKGFTSLQRFAPTQSQFYH  
LFLHGNSLTRLFPNEFANFYNAVSLHMENGLHEIVPGAFLGLQLVKRLHINNNKIKSFRKQ  
TFLGLDDLEYLQADFNLLRDIDPGAQDLNKLVLILNDNLISTLPANVFQYVPITHLDLRG  
NRLKTLPLYEEVLEQIPGIAEILLEDNPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ  
GKDLNETTEQDLCPLKNRVDSSLPAPPAQEETFAPGPLPTPFKTNGQEDHATPGSAPNGGTK  
IPGNWQIKIRPTAAIATGSSRNKPLANSILPCPGGCSCDHIPGSGLMNCNNRVSSLADLKP  
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLLDLRWLYMDSNY  
LDTLSREKFAGLQNLLEYLNVEYNAIQILIPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSL  
SKLSLHNNYFMYLPVAGVLDQLTSIIQIDLHGPNWECSTIVPFKQWAERLGSEVLMSDLKC  
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL  
VPGLLLVFVTSFTVVGMLVFILRNKRKSKRRDANSSASEINSLQTVCDSSYWHNGPYNADG  
AHRVYDCGSHSLSD

### **Signal sequence:**

amino acids 1-15

### **Transmembrane domain:**

amino acids 618-638

### **N-glycosylation site.**

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 122-126, 646-650

### **Casein kinase II phosphorylation site.**

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577, 608-612, 657-661, 666-670, 693-697

### **N-myristoylation site.**

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349, 354-360, 465-471, 493-499, 598-604, 603-609

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 337-348

## FIGURE 35

AGTCGACTGCGTCCCCCTGTACCCGGCGCCAGCTGTGTTCCCTGACCCCAGAATAACTCAGGGC  
TGCACCGGGCCTGGCAGCGCTCCGCACACATTTCTGTGTCGCGGCCTAAGGGAAACTGTTGGC  
CGCTGGGCCCCGCGGGGGGATTCTTGGCAGTTGGGGGGTCCGTGCGGGAGCGAGGGCGGAGGGG  
AAGGGAGGGGGAACCGGGTTGGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC  
AGCTCTGCGTCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCGGGGCCCTCAG  
AGAATGAGGCCCGCGTTCGCCCTGTGCCTCCTCTGGCAGGCGCTCTGGCCCCGGGCCGGGCGG  
CGGCGAACACCCCCACTGCCGACCGTGCTGGCTGCTCGGCCTCGGGGGCCTGCTACAGCCTGC  
ACCACGCTACCATGAAGCGGCAGGCGGCCGAGGAGGCCTGCATCCTGCGAGGTGGGGCGCTC  
AGCACCGTGCGTGCGGGCGCCGAGCTGCGCGCTGTGCTCGCGCTCCTGCGGGCAGGCCCAGG  
GCCCCGAGGGGGCTCCAAAGACCTGCTGTTCTGGGTGCGACTGGAGCGCAGGCGTTCCCACT  
GCACCTTGGAGAACGAGCCTTTGCGGGGTTTCTCCTGGCTGTCTCCGACCCCCGGCGGTCTC  
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGCGGAGATGCGC  
GGTACTCCAGGCCACCGGTGGGGTCGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC  
GCGCCAACGGCTACCTGTGCAAGTACCAGTTTGAGGTCTTGTTGTCTGCGCCGCGCCCCGGG  
GCCGCTCTAACTTGAGCTATCGCGCGCCCTTCCAGCTGCACAGCGCCGCTCTGGACTTCAG  
TCCACCTGGGACCGAGGTGAGTGCGCTCTGCCGGGGACAGCTCCCGATCTCAGTTACTTGCA  
TCGCGGACGAAATCGGCGCTCGCTGGGACAACTCTCGGGCGATGTGTTGTGTCCCTGCCCC  
GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAACTGCCTAGACGACTTGGGAGG  
CTTTGCCTGCGAATGTGCTACGGGCTTCGAGCTGGGGAAGGACGGCCGCTCTTGTTGTGACCA  
GTGGGGAAGGACAGCCGACCCTTGGGGGGACCGGGGTGCCACCAGGCGCCCGCCGGCCACT  
GCAACCAGCCCCGTGCCGACAGAAACATGGCCAATCAGGGTCGACGAGAAGCTGGGAGAGAC  
ACCACTTGTCCCTGAACAAGACAATTAGTAACATCTATTCTGAGATTCTTCGATGGGGAT  
CACAGAGCACGATGTCTACCCTTCAAATGTCCCTTCAAGCCGAGTCAAAGGCCACTATCACC  
CCATCAGGGAGCGTGATTTCCAAGTTTAATTCTACGACTTCCTCTGCCACTCCTCAGGCTTT  
CGACTCCTCCTCTGCCGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTGGTGATCT  
TGACCATGACAGTACTGGGGCTTGTCAAGCTCTGCTTTCACGAAAGCCCCTCTTCCCAGCCA  
AGGAAGGAGTCTATGGGCCCCGCGGGCCTGGAGAGTGATCCTGAGCCCGCTGCTTTGGGCTC  
CAGTTCTGCACATTGCACAAACAATGGGGTGAAAGTCGGGGACTGTGATCTGCGGGACAGAG  
CAGAGGGTGCCCTTGCTGGCGGAGTCCCCTCTTGGCTCTAGTGATGCATAGGGAAACAGGGGA  
CATGGGCACTCCTGTGAACAGTTTTTCACTTTTGATGAAACGGGGAACCAAGAGGAACTTAC  
TTGTGTAACCTGACAATTTCTGCAGAAATCCCCCTTCTCTAAATTCCCTTTACTCCACTGAG  
GAGCTAAATCAGAACTGCACACTCCTTCCCTGATGATAGAGGAAGTGGAAGTGCCTTTAGGA  
TGGTGATACTGGGGGACCGGGTAGTGCTGGGGAGAGATATTTTCTTATGTTTATTCCGAGAA  
TTTGGAGAAGTGATTGAACTTTTCAAGACATTGGAACAAATAGAACACAATATAATTTACA  
TTAAAAAATAATTTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTTTCTAGGCTAGGAGTAT  
ATTGGTTTCGAAATCCCAGGGAAAAAATAAAAAATAAAAAATTAAAGGATTGTTGAT

“CTT”-5640660

## **FIGURE 36**

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAEEACILRGGALS  
TVRAGAE LRAVLALLRAGPGPGGSKDLLFWVALERRRSHCTLENEPLRGFSWLSSDPGGLE  
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLC PAPRPGA  
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG  
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTS GEGQPTLGGTGVPTRRPPATA  
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP  
SGSVISKFNSTTSSATPQAFDSSSAVVFI FVSTAVVVLVILTMTVLGLVKLCFHESPSSQPR  
KESMGPPGLESDPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 399-418

### **N-glycosylation site.**

amino acids 189-193, 381-385

### **Glycosaminoglycan attachment site.**

amino acids 289-293

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 98-102, 434-438

### **Casein kinase II phosphorylation site.**

amino acids 275-279, 288-292, 342-346, 445-449

### **N-myristoylation site.**

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,  
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,  
477-483

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 262-274



## FIGURE 37

CGGACGCGTGGGATTAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG  
CGTCGAGTCAGACGGCACCATAATCGCCTTTAAAAGTGCCTCCGCCCTGCCGGCCGCGTATC  
CCCCGGCTACCTGGGCGCGCCCGCGGCGGTGCGCGCGTGAGAGGGAGCGCGCGGGCAGCCGA  
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGGCGGTGTGAGCGCGGTGGGTGCGGA  
GGGGCGTGTGTGCCGGCGCGCGCGCCGTGGGGTGCAAACCCGAGCGTCTACGCTGCCATGA  
GGGGCGCGAACGCCTGGGCGCCACTCTGCCTGCTGCTGGCTGCCGCCACCCAGCTCTCGCGG  
CAGCAGTCCCCAGAGAGACCTGTTTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT  
TATTGGCAGTGAAGGTTTTCTGGAGTGTACCCTCCAAATAGCAAATGTACTTGGAAAATCA  
CAGTTCCCGAAGGAAAAGTAGTCGTTCTCAATTTCCGATTTCATAGACCTCGAGAGTGACAAC  
CTGTGCCGCTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGGCCAGCGCATTGGCCG  
CTTCTGTGGCACTTTCCGGCCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA  
TGATTTCTGATGCCAACACAGCTGGCAATGGCTTCATGGCCATGTTCTCCGCTGCTGAACCA  
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTTCCGGCTCTTTTAAAC  
CCCCAACTGGCCAGACCGGGATTACCCTGCAGGAGTCACTTGTGTGTGGCACATTGTAGCCC  
CAAAGAATCAGCTTATAGAATTAAAGTTTGAGAAGTTTGATGTGGAGCGAGATAACTACTGC  
CGATATGATTATGTGGCTGTGTTTAATGGCGGGGAAGTCAACGATGCTAGAAGAATTGGAAA  
GTATTGTGGTGATAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACTTCTTATTAGT  
TTTTATCAGACTTAAGTTTAACTGCAGATGGGTTTTATTGGTCACTACATATTCAGGCCAAAA  
AAACTGCCTACAACACAGAACAGCCTGTCAACCACCATTCCTGTAACCACGGGTTTTAA  
ACCCACCGTGGCCTTGTGTCAACAAAAGTGTAGACGGACGGGGACTCTGGAGGGCAATTATT  
GTTCAAGTGACTTTGTATTAGCCGGCACTGTTATCACAAACCATCACTCGCGATGGGAGTTTG  
CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTTGGCGATTACAGCAGCGGG  
CAAGAACATGAGTGCCAGGCTGACTGTCTGCAAGCAGTGCCCTCTCCTCAGAAGAGGTC  
TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGGCGAGGCAAATCATGCCAACAGC  
TTTATCATGATGTTCAAGACCAAGAATCAGAAGCTCCTGGATGCCTTAAAAAATAAGCAATG  
**TTAA**CAGTGAAGTGTGTCCATTTAAGCTGTATTCTGCCATTGCCTTTGAAAGATCTATGTTT  
TCTCAGTAGAAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG  
GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAGTTCTT  
TGCCTGCTGTGAGAGGAGCAGCTATCTGATTGGAACCTGCCGACTTAGTGCGGTGATAGGA  
AGCTAAAAGTGTCAAGCGTTGACAGCTTGGAAGCGTTTATTTATACATCTCTGTAAAAGGAT  
ATTTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAGATTTTAGAAGTGCAATATTTATAGT  
GTTATTTGTTTCACTTCAAGCCTTTGCCCTGAGGTGTTACAATCTTGTCTTGCGTTTTCTA  
AATCAATGCTTAATAAAATATTTTTTAAAGGAAAAAAAAAAAA

1044 10 95640666

## **FIGURE 38**

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK  
ITVPEGKVVLNFRFIDLESNDLCRYDFVDVYNHANGQRIGRFCGTFRPGALVSSGNKMMV  
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV  
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPPAPIVSEARNELLI  
QFLSDLSLTADGFIGHYIFRPKKLPPTTTEQPVTTTTFPVTTGLKPTVALCQQKCRRTGTLEGN  
YCSSDFVLAGTVITTTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR  
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

### **Signal sequence:**

amino acids 1-23

### **N-glycosylation site.**

amino acids 355-359

### **Casein kinase II phosphorylation site.**

amino acids 64-68, 142-146, 274-278

### **Tyrosine kinase phosphorylation site.**

amino acids 199-208

### **N-myristoylation site.**

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,  
305-311, 309-315, 320-326, 330-336

### **Cell attachment sequence.**

amino acids 149-152

## FIGURE 39

CGGACGCGTG GGGCGGACGCGTG GGGCGGCCACGGCGCCCGCGGGCTGGGGCGGTGCGTTCTT  
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAGATGGGCCCCATGGCCCCGAAGG  
GCCTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCTCAACCTCCCAGGACCTATCTGG  
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCCGCCTCAGCCCCATCCGTGTCATACCTG  
CCGGGGACTGGTTGACAGCTTTAACAAGGGCCTGGAGAGAACCATCCGGGACAACTTTGGAG  
GTGGAAACACTGCCTGGGAGGAAGAGAATTTGTCCAAATACAAAGACAGTGAGACCCGCCTG  
GTAGAGGTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT  
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTTCACAAGCAGCAGGAGGCCCCGGACCTCTTCC  
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCCGCAGGCACCTTCGGGGCCCTCCTGC  
CTTCCCTGTCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGG  
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCC  
AGTGTGGCCTTGGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTTCGGCTTGT  
TTTGGCCCCGTGCCCCGATGCTCAGGACCTGAGGAATCAAACCTGTTTGCAATGCAAGAAGGG  
CTGGGCCCTGCATCACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAACT  
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG  
GCCTGCCTAGGCTGCATGGGGGCAGGGCCAGGTCGCTGTAAGAAGTGTAGCCCTGGCTATCA  
GCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGA  
ACAAGCAGTGTGAAAACACCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG  
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC  
AGAAGACGAGTTGGTGGTGTGCTGCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCA  
CGCTGGCTGCTAAGGGCGACTTGGTGTTCACCGCCATCTTCATTGGGGCTGTGGCGGCCATG  
ACTGGCTACTGGTTGTCAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATTA  
ATCGCGGCCACCACCTGTAGGACCTCCTCCCACCCACGCTGCCCCCAGAGCTTGGGCTGCCC  
TCCTGCTGGACACTCAGGACAGCTTGGTTTATTTTTGAGAGTGGGGTAAGCACCCCTACCTG  
CCTTACAGAGCAGCCCAGGTACCCAGGCCCGGGCAGACAAGGCCCTGGGGTAAAAAGTAGC  
CCTGAAGGTGGATAACCATGAGCTCTTCACCTGGCGGGGACTGGCAGGCTTCACAATGTGTGA  
ATTTCAAAGTTTTTTCCTTAATGGTGGCTGCTAGAGCTTTGGCCCCCTGCTTAGGATTAGGTG  
GTCCTCACAGGGGTGGGGCCATCACAGCTCCCTCCTGCCAGCTGCATGCTGCCAGTTCCTGT  
TCTGTGTTACCCACATCCCCACACCCCATTGCCACTTATTTATTCATCTCAGGAAATAAAGA  
AAGGTCTTGAAAGTTAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 40**

MAPWPPKGLVPAVLWGLSLFLNLPGPILWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER  
TIRDNFGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ  
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGQCEGEGTRGGSGHCDCQAG  
YGGEACGQCGLGYFEAERNASHLVCSACFGPCARCSGPESNCLQCKKGWALHHLKCVDIDE  
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE  
TEVCPGENKQCENTEGGYRCICAEGYQMEGICVKEQIPESAGFFSEMTEDLVVLQQMFFG  
IIICALATLAAKGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

### **Signal sequence:**

amino acids 1-29

### **Transmembrane domain:**

amino acids 372-395

### **N-glycosylation site.**

amino acids 79-83, 205-209

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 290-294

### **Casein kinase II phosphorylation site.**

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

### **N-myristoylation site.**

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,  
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,  
326-332, 372-378, 395-401

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 321-333

### **EGF-like domain cysteine pattern signature.**

amino acids 181-193

## FIGURE 41

TGAGACCCCTCCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA  
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGCACTCTGGGTGTTGCCCCTGGCCAGCCCCGGG  
GCCGCCCTGACCGGGGAGCAGCTCCTGGGCAGCCTGCTGCGGCAGCTGCAGCTCAAAGAGGT  
GCCCACCCCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCCAGT  
ACGTGGCCCTGCTGCAGCGCAGCCACGGGGACCGCTCCCGCGGAAAGAGGTTTACGCCAGAGC  
TTCCGAGAGGTGGCCGGCAGGTTTCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGTTCGG  
CATGGAGCAGCGGCTGCCGCCCAACAGCGAGCTGGTGCAGGCCGTGCTGCGGCTCTTCCAGG  
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGGCGGCTGTCCCCGCGCAGCGCCCGGGCC  
CGGGTGACCGTTCGAGTGGCTGCGCGTCCGCGACGACGGCTCCAACCGCACCTCCCTCATCGA  
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA  
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG  
GAGCATCTGGGCCCCGCTGGCGTCCGGCGCCCAAGCTGGTCCGCTTTGCCTCGCAGGGGGC  
GCCAGCCGGGCTTGGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTTGGGGACTATGGAG  
CTCAGGGCGACTGTGACCCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG  
ATGTACATTGACCTGCAGGGGATGAAGTGGGCCGAGAACTGGGTGCTGGAGCCCCCGGGCTT  
CCTGGCTTATGAGTGTGTGGGCACCTGCCGGCAGCCCCCGGAGGCCCTGGCCTTCAAGTGGC  
CGTTTCTGGGGCCTCGACAGTGCATCGCCTCGGAGACTGACTCGCTGCCCATGATCGTCAGC  
ATCAAGGAGGGAGGCAGGACCAGGCCCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA  
GTGCAGCTGTGCCTCGGATGGTGCGCTCGTGCCAAGGAGGCTCCAGCCATTAGGCGCCTAGTG  
TAGCCATCGAGGGACTTGACTTGTGTGTGTTTCTGAAGTGTTTCGAGGGTACCAGGAGAGCTG  
GCGATGACTGAACTGCTGATGGACAAATGCTCTGTGCTCTCTAGTGAGCCCTGAATTTGCTT  
CCTCTGACAAGTTACCTCACCTAATTTTTGCTTCTCAGGAATGAGAATCTTTGGCCACTGGA  
GAGCCCTTGCTCAGTTTTTCTATTCTTATTATTCACTGCACTATATTCTAAGCACTTACAT  
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCANTGTGTCAATTGTTTACTTGTCTGTAC  
TGATCTGGGCTAAAGTCCTCCACCACCACTCTGGACCTAAGACCTGGGGTTAAGTGTGGGT  
TGTGCATCCCCAATCCAGATAATAAAGACTTTGTAAAACATGAATAAAACACATTTTATTCT  
AAAA

## **FIGURE 42**

MQPLWLCWALWVLPLASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV  
ALLQRSHGDRSRGKRFSQSFREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP  
VPKAALHRHGRSLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF  
WQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ  
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCTCRQPPEALAFKWPF  
LGPRQCIASETDSLPMIVSIKEGGTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

### **Signal sequence:**

amino acids 1-18

### **N-glycosylation site.**

amino acids 158-162

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 76-80

### **Casein kinase II phosphorylation site.**

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

### **N-myristoylation site.**

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

### **Amidation site.**

amino acids 74-78

### **TGF-beta family signature.**

amino acids 282-298

## FIGURE 43

GTCTGTTCCCAGGAGTCCTTCGGCGGCTGTTGTGTGTCAGTGGCCTGATCGCGATGGGGACAAA  
GGCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG  
CATTGGGCAGTGTTACAGTGCACCTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT  
GTGAAGTTGTCCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAGTTTGACCA  
AGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG  
TGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC  
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT  
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCCTCCTCTGCCACCATTGGGAACCGGG  
CAGTGCTGACATGCTCAGAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGAT  
GGGATAGTGATGCCTACGAATCCCAAAGCACCCTGTCCTTCAGCAACTCTTCCTATGTCCT  
GAATCCCACAACAGGAGAGCTGGTCTTTGATCCCCCTGTCAGCCTCTGATACTGGAGAATACA  
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT  
GTGGAGCGGAATGTGGGGGT CATCGTGGCAGCCGTCTTGTAACCCTGATTCTCCTGGGAAT  
CTTGGTTTTTTGGCATCTGGTTTTGCCTATAGCCGAGGCCACTTTGACAGAACAAAGAAAGGGA  
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG  
ACCTCGTCATTCTTGGTGTGAGCCTGGTCTGGCTCACCGCCTATCATCTGCATTTGCCTTACT  
CAGGTGCTACCGGACTCTGGCCCCCTGATGTCTGTAGTTTCACAGGATGCCTTATTTGTCTTC  
TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCC  
ATCCTCCTTCATGCCCTCCCTCCCTTTTCTTACCCTGCTGAGTGGCCTGGAACCTGTTTAA  
GTGTTTATTCCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC  
TTCTAAGTAGACAGCAAAAATGGCGGGGGTCTGCAGGAATCTGCACTCAACTGCCACCTGGC  
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGGTTCTGGGCTCTTTCCTTGTGTACTGAC  
GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGG  
TGATGACACTGGGGTCCTTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTG  
CCACTGGGATCCCTCTGCCCTGTCCTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGT  
GGAAAATGGGAGCTCTTGTGTGGAGAGCATAGTAAATTTTCAGAGAACTTGAAGCCAAAAG  
GATTTAAAACCGCTGCTCTAAAGAAAAGAAAACCTGGAGGCTGGGCGCAGTGGCTCACGCCTG  
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTCTGGGAGTTCGGGATCAGCCTGACCA  
ACATGGAGAAACCTTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC  
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

## **FIGURE 44**

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRVEW  
KFDQGDTTTRLVCYNNKITASYEDRVTFLLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKV  
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPEYTWFKDGIVMPTNPKSTRAFSNS  
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVA AVLVTLI  
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

### **Signal sequence:**

amino acids 1-27

### **Transmembrane domain:**

amino acids 238-255

### **N-glycosylation site.**

amino acids 185-189

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 270-274

### **Casein kinase II phosphorylation site.**

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,  
193-197, 203-207, 287-291

### **N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262



## FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGA  
GCGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTGCTCGGCCTCGGACTAGGCCT  
GGAGGCCGCGCGAGCCCGCTTTCACCCCGACCTCTGCCCAGGCCGCAGGCCCCAGCTCAG  
GCTCGTGCCCACCCACCAAGTTCCAGTGCCGCACCAGTGGCTTATGCGTGCCCCCTCACCTGG  
CGCTGCGACAGGGACTTGGA CTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC  
ATGTACCCAGAAAGGGCAATGCCCACCGCCCCCTGGCCTCCCCTGCCCCCTGCACCGGCGTCA  
GTGACTGCTCTGGGGGAACTGACAAGAACTGCGCAACTGCAGCCGCCTGGCCTGCCTAGCA  
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA  
CCCAGACTGTCCCGACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGGAAG  
GGGATGCCACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTACCTCTCTCAGGAATGCC  
ACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTCCCCTCTGTGCGGAATGCCACATCCTC  
CTCTGCCGGAGACCAGTCTGGAAGCCCCAACTGCCTATGGGGTTATTGCAGCTGCTGCGGTGC  
TCAGTGCAAGCCTGGTCAACGCCACCCTCCTCCTTTTGTCTGGCTCCGAGCCCAGGAGCGC  
CTCCGCCCCACTGGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTCAGAACAGAAGAC  
CTCGCTGCCCTGAGGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACA  
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT  
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC  
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGGAACCTGCCACAGCCAGAACTGAG  
GGGCTGGCCCCAGGCAGCTCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG  
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

## **FIGURE 46**

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR  
TSGLCVPLTWRCDRDLDCSDGSDEEEECRIEPCCTQKGQCPPPPGLPCPCTGVSDCSGGTDKKL  
RNCSRLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELGCGTNEILPEGDATTMGPPVT  
LESVTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAVLSASLVTATLL  
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

### **Signal sequence:**

amino acids 1-30

### **Transmembrane domain:**

amino acids 230-246

### **N-glycosylation site.**

amino acids 126-130, 195-199, 213-217

### **Casein kinase II phosphorylation site.**

amino acids 84-88, 140-144, 161-165, 218-222

### **N-myristoylation site.**

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,  
224-230, 230-236, 263-269

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 44-55

### **Leucine zipper pattern.**

amino acids 17-39

## FIGURE 47

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTGCGGCACAGATGCGG  
GTTAGACTGGCGGGGGGAGGAGGCGGAGGAGGGAAGGAAGCTGCATGCATGAGACCCACAGA  
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG  
GAGATGGATTTCTAGAGCAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG  
GCCGTGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTT  
CGATGACCTTCAAGTGTGTGCTGACCCCGGCATTCCCGAGAATGGCTTCAGGACCCCCAGCG  
GAGGGGTTTTCTTTGAAGGCTCTGTAGCCCGATTTCACTGCCAAGACGGATTCAAGCTGAAG  
GGCGCTACAAAGAGACTGTGTTTGAAGCATTTTAATGGAACCTAGGCTGGATCCCAAGTGA  
TAATTCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCATA  
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTTCATGAAGGATTCAAGATCCGG  
TACCCCGACCTACACAATATGGTTTCATTATGTGCGGATGATGGAACGTGGAATAATCTGCC  
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGC  
TCCAGACCTCCTTCCCGGTGGGGACTGTGATCTCCTATCGCTGCTTTCCCGGATTTAAACTT  
GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCCACCCCGGTG  
CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTTCGTCT  
GCCACCCGCGGCCTTGTGAGCGCTACAACCACGGAAGTGTGGTGAGTTTTACTGCGATCCT  
GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTTCTTC  
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCCAGCACCCATGAGACCCTCCTGA  
CCACGTGGAAGATTGTGGCGTTACCGCAACCAAGTGTGCTGCTGGTGCTGCTGCTGCTCATC  
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCCACTTTCCCCCAGGGGGCCTCCCCGAG  
TTCCAGCAGTGACCCTGACTTTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCCTATG  
ACGAAGCTGTGAGTGGCGGCTTGAGTGCTTAGGCCCCGGGTACATGGCCTCTGTGGGCCAG  
GGCTGCCCCTTACCCGTGGACGACCAGAGCCCCCAGCATACCCCGGCTCAGGGGACACGGA  
CACAGGCCCAGGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAA  
GTCTGTATTACCTCCCAGGTGCCAAGAGAGCACCCACCCTGCTTCGGACAACCTGACATA  
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCAGGCATCCATCATGCCCACTGGGT  
GTTGTTCCCTAAGAAACTGATTTGATTAAAAAATTTCCCAAAGTGTCTCTGAAGTGTCTCTTCAA  
ATACATGTTGATCTGTGGAGTTGATTCTTTCTTCTTGGTTTTAGACAAATGTAAACAA  
AGCTCTGATCCTTAAAAATTGCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTC  
CTGTTTCTTCTTGACACAGACTGATTAAAAATTAAAAGNAAAAA

## **FIGURE 48**

MYHGMNPSNGDGFLEQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI  
PENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI  
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS  
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPPRCLALEAQVCPLP  
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT  
WPSTHETLLTTWKIVAFTATSULLVLLLVILARMFQTKFAHFPPRGPPRSSSSDPDFVVVD  
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGD TDTGPGESETCDS  
VSGSSELLQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWVLFRLN

### **Signal sequence:**

amino acids 1-41

### **Transmembrane domain:**

amino acids 325-344

### **N-glycosylation site.**

amino acids 104-108, 134-138, 192-196

### **Casein kinase II phosphorylation site.**

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,  
364-368, 380-384, 467-471, 468-472

### **N-myristoylation site.**

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,  
478-484

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405

## FIGURE 49

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGCGGTCCGTCGGTGGCCTAGAGA  
TGCTGCTGCCGCGGTTGCAGTTGTGCGGCACGCCTCTGCCCCGCCAGCCCGCTCCACCGCCGT  
AGCGCCCGAGTGTCGGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGGAACCGCGCTACAGG  
CCGTGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGCGACGGGTGCGCTGCTGAGTGCC  
TCGGATTTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGGAGGGACACAGAGGCCTTGTTA  
TAAAGTCATTTACTTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAGAAGCCT  
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAACTGATAGAA  
AAGTTCATTGAAAACCTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGA  
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGGAATGATGGCAGCATAT  
CACAAATTTAGGAACTGGTATGTGGATGAGCCGTCTGCGGCAGCGAGGTCTGCGTGGTCATG  
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAATGATGA  
CCGGTGCAACATGAAGAAACAATTTCAATTTGCAAATATTCTGATGAGAAACCAGCAGTTCCTT  
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG  
GAAGAAGATGCCAAAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACAT  
CCTAATCCCCAGCATTCCCCTTCTCCTCCTCCTTGTGGTCACCACAGTTGTATGTTGGGTTT  
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCTTAGCACAAAGAAGCAACACACCATC  
TGGCCCTCTCCTCACCAGGGAAACAGCCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA  
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTTCAATCCGAGTGTGTT  
CGGGAGAAGCCACTCCCGATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCA  
GAAAGTGGGTTTGTGACTCTGGTGAGCGTGGAGAGTGGATTGTGACCAATGACATTTATGA  
GTTCTCCCCAGACCAAATGGGGAGGAGTAAGGAGTCTGGATGGGTGGAAAATGAAATATATG  
GTTATTAGGACATATAAAAACTGAACTGACAACAATGGAAAAGAAATGATAAGCAAAATC  
CTCTTATTTTCTATAAGGAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCCTGT  
GGATGAGCATGTGGTCCCCACGACCTCCTGTTGGACCCCCACGTTTTGGCTGTATCCTTTAT  
CCCAGCCAGTCATCCAGCTCGACCTTATGAGAAGGTACCTTGCCCAGGTCTGGCACATAGTA  
GAGTCTCAATAAATGTCACCTGGTTGGTTGTATCTAACTTTTAAGGGACAGAGCTTTACCTG  
GCAGTGATAAAGATGGGCTGTGGAGCTTGAAAACACCTCTGTTTTCTTGCTCTATACAG  
CAGCACATATTATCATAACAGACAGAAAATCCAGAATCTTTTCAAAGCCACATATGGTAGCACAG  
GTTGGCCTGTGCATCGGCAATTCTCATATCTGTTTTTTCAAAGAATAAAATCAAATAAAGA  
GCAGGAAAAAAA

Figure 1: Schematic representation of the experimental design. The figure shows a vertical timeline of events. At the top, 'Pre-Test' is indicated. Below it, 'Training' is shown with a box labeled 'Training' and a sub-label 'Training' below it. This is followed by 'Post-Test' and 'Follow-Up' phases. The timeline is divided into 'Pre-Test', 'Training', 'Post-Test', and 'Follow-Up' sections. The 'Training' section is further divided into 'Training' and 'Training' sub-sections. The 'Post-Test' section is divided into 'Post-Test' and 'Post-Test' sub-sections. The 'Follow-Up' section is divided into 'Follow-Up' and 'Follow-Up' sub-sections. The timeline is marked with 'Time' on the right side.

Signal sequence:

**Transmembrane domain:**

N-glycosylation site.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Casein kinase II phosphorylation site.

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

## FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGC  
ATCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT  
GTTTGCCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT  
GTTTACGATGCGCTTGTGGACCCAGTGGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACC  
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGC  
CTGCTGAAGTTGAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCC  
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCCAAACCTC  
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT  
CAATACCATGAGACCACCCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTGGGCAT  
GCAGCAAATGTTTGCCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTC  
TTTACCAACCTTCAACCCACAGGAGGTCTTTATTTCGTTCCACTAACATTTTTTCGGAATCTG  
GAGTCCACCCGTTGTTTGCTGGCTGGGCTTTTCCAGTGTGAGAAAGAAGGACCCATCATCAT  
CCACACTGATGAAGCAGATTCAGAAGTCTTGTATCCCAACTACCAAAGCTGCTGGAGCCTGA  
GGCAGAGAACCAGAGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTTG  
AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCT  
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTTG  
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGTACATACTGCCCAAGGAAGACAGG  
GAAAGTCTTCAGATGGCAGTAGGCCCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGC  
CATGGACTCTGCCACTGCCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG  
TGACCTTCATACCGCTCTTAATGACCCTGGGGATTTTTGACCACAAATGGCCACCGTTTGCT  
GTTGACCTGACCATGGAACCTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTA  
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGT  
TCTTGAATGCCATGTCAGTTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA  
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTTATAAAAGCAGGATGTGTTGATT  
TTAAAATAAAGTGCCTTTATACAATG

## **FIGURE 52**

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMOVVFRHGAR  
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL  
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE  
GPIIIHTDEADSEVLYPNYQSCWSLRQRTGRRRQTASLQPGISEDLLKKVKDRMGIDSSDKVD  
FFILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFHLHILES  
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLMLTGLIFDHKWPPFAVDLTMELYQHLESKEW  
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMS SVYTLSP EKYHALCSQTQVMEVGNEE

### **Signal sequence:**

amino acids 1-23

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 218-222

### **Casein kinase II phosphorylation site.**

amino acids 87-91, 104-108, 320-324

### **Tyrosine kinase phosphorylation site.**

amino acids 280-288

### **N-myristoylation site.**

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

### **Amidation site.**

amino acids 216-220

### **Leucine zipper pattern.**

amino acids 10-32

### **Histidine acid phosphatases phosphohistidine signature.**

amino acids 50-65



## FIGURE 53

CTCCTCTTAACATACTTGCAGCTAAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT  
TAAATTTTCAGCTCATCACCTTCACCTGCCTTGGTCAATGGCTCTGCTATTCTCCTTGATCCTT  
GCCATTTGCACCAGACCTGGATTCCCTAGCGTCTCCATCTGGAGTGCGGCTGGTGGGGGGCCT  
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGTGATG  
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGTGCCGGGAGCTGGGCTGTGGAGCTGCCAGC  
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCCTCATCCA  
ATCAGTCAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG  
ATTGTTACATGATGAAGATGCTGGGGCATCGTGTGAGAACCCAGAGAGCTCTTTCTCCCCA  
GTCCCAGAGGGTGTGAGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAAGTGAA  
GCACCAGAACCAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCCGCAAAGGTGG  
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC  
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCTTCA  
GGATTGCCCTTCTGGGCCTTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGGTGC  
AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG  
GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAACCTGGGGAGAAAAGGAGGA  
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCTTCAGAGACCGGA  
AATGCTATGGCCCTGGGGTTGGCCGCATCTGGCTGGATAATGTTGCTCAGGGGAGGAG  
CAGTCCCTGGAGCAGTGCCAGCACAGATTTTGGGGGTTTCACGACTGCACCCACCAGGAAGA  
TGTGGCTGTCATCTGCTCAGTGTAGGCTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA  
GAAAAACACAGAAGAAGGGAGCATTTACTGTCTACATGACTGCATGGGATGAACACTGATCT  
TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCTGATTCTCAGGCCTTCAGAGTTGG  
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTTGGAACTACATCA  
CCACCTTTCCTATGTCTCCACATTGCACACAGCAGATTCCCAGCCTCCATAATTGTGTGTAT  
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACACATA  
CACCATTTGTCTGTTTCTCTGAAGAAGTCTGACAAAATACAGATTTTGGTACTGAAAGAGA  
TTCTAGAGGAACGGAATTTTAAGGATAAATTTTCTGAATTGGTTATGGGGTTTCTGAAATTG  
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACTTTATTTACAATAATAAGATAGCAC  
TATGTGTTCAA

## **FIGURE 54**

MALLFSLILAICTRPGFLASPSGVRLVGGLHRCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC  
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC  
ENPESFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCTGWSLRAAKVVCRQLGCGRAVL  
TQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG  
GDNLCSGRLEVLHKGWGSVCDDNWGEKEDQVVKQLGCGKSLSPSFRDRKCYGPGVGRIWL  
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

### **Signal sequence:**

amino acids 1-15

### **Casein kinase II phosphorylation site.**

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,  
267-271, 294-298, 316-320, 336-340

### **N-myristoylation site.**

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,  
180-186, 263-269, 286-292

### **Amidation site.**

amino acids 196-200

### **Speract receptor repeated domain signature.**

amino acids 29-67, 249-287

## FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC  
CCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG  
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTTCGGCTGCCTGGG  
CGTCTTCGGCCTCTTCCGGCTGCTGCAGTGGGTGCGCGGGAAGGCCTACCTGCGGAATGCTG  
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGGCAAAGAATGTGCAAAAGTCTTCTATGCT  
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAATGGTGGGGCCCTAGAAGAGCTCATCAGAGA  
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC  
TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTTGGCTATGTC  
GACATACTTGTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGGA  
TGTGGACAAGAGGGTCATGGAGACAACTACTTTGGCCCAGTTGCTCTAACGAAAGCACTCC  
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTGCGCCATCAGCAGCATCCAGGGCAAG  
ATGAGCATTCTTTTTGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTTCTTTGA  
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA  
TCCACACCAACCTCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC  
ACCACCACAGCCCAGGGCCGAAGCCCTGTGGAGGTGGCCCAGGATGTTCTTGCTGCTGTGGG  
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCCTTGGCTGTTTATCTTCGAA  
CTCTGGCTCCTGGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC  
AAGAACTCCTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC  
TTACTCTACAAGGGACAGTTGCATTTGTTGAGACTTTAATGGAGATTTGTCTCACAAGTGGG  
AAAGACTGAAGAAACACATCTCGTGACATCTGCTGGCAGAGGACAATCAAAAACGACAACA  
AGCTTCTTCCCAGGGTGAGGGGAAACACTTAAGGAATAAATATGGAGCTGGGGTTTAACACT  
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAG  
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTTTATTGCAGCTTATAATGGTTAC

## **FIGURE 56**

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGA  
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEILQCFGYVDIL  
VNNAGISYRGTIMDTTVDVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAIISSIQ GKMSI  
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT  
AQGRSPVEVAQDVLAAVGKKKKDVILADLLPSLAVYLR TLAPGLFFSLMASRARKERKSKNS

### **Signal sequence:**

amino acids 1-21

### **Transmembrane domain:**

amino acids 104-120, 278-292

### **N-glycosylation site.**

amino acids 228-232

### **Glycosaminoglycan attachment site.**

amino acids 47-51

### **Casein kinase II phosphorylation site.**

amino acids 135-139, 139-143, 253-257

### **Tyrosine kinase phosphorylation site.**

amino acids 145-153, 146-153

### **N-myristoylation site.**

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

### **Amidation site.**

amino acids 265-269

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 6-17

101120-95640000

## FIGURE 57

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA  
AAAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTTCTTCTGGACATCCTC  
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTTCGTGAAGCTTTTTATTCTTAA  
GAGGAGAAAATCAGTCACCGGCGAAATCGTGCTGATTACAGGAGCTGGGCATGGAATTGGGA  
GACTGACTGCCTATGAATTTGCTAAACTTAAAAGCAAGCTGGTTCTCTGGGATATAAATAAG  
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTTCATACCTTTGT  
GGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG  
GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGCTACA  
CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGCACATTTCTGGACTACAAA  
GGCATTCTCTCCTGCAATGACGAAGAATAACCATGGCCATATTGTCACGTGTGGCTTCGGCAG  
CTGGACATGTCTCGGTCCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGCTGCTGTTGGA  
TTTCATAAACTTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG  
TCTGTGTCCTAATTTTCGTAAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA  
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG  
ATTTTTATTCCATCTTCTATAGCTTTTTTAAACAACATTGGAAAGGATCCTTCCTGAGCGTTT  
CCTGGCAGTTTTTAAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATTGGATATAAAATGA  
AAGCGCAATAAGCACCTAGTTTTCTGAAAACCTGATTTACCAGGTTTAGGTTGATGTCATCTA  
ATAGTGCCAGAATTTTAATGTTTGAACCTCTGTTTTTTCTAATTATCCCCATTTCTTCAATA  
TCATTTTTTGAGGCTTTGGCAGTCTTCATTTACTACCACCTGTTCTTTAGCCAAAAGCTGATT  
ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAAGAA  
CCAAAATGACTTTATTAAATAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA  
AATTTGTACCATAACCGTTTATTTAACATATATTTTTATTTTTTGATTGCACTTAAATTTTGT  
ATAATTTGTGTTTCTTTTTCTGTTCTACATAAAATCAGAACTTCAAGCTCTCTAAATAAAA  
TGAAGGACTATATCTAGTGGTATTTCACAATGAATATCATGAACTCTCAATGGGTAGGTTTC  
ATCCTACCCATTGCCACTCTGTTTCTGAGAGATACCTCACATTCCAATGCCAAACATTTCT  
GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTTAAG  
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA  
AA  
AA

## **FIGURE 58**

MKFLLDILLLLPLLVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK  
LVLWDINKHGLEETAACKGLGAKVHTFVVDCSNREDIYSSAKKVKAIEIGDVSILVNNAGVV  
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHI VTVASAAGHVSVFPFLAYC  
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMH  
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

### **Signal sequence:**

amino acids 1-19

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-34, 283-287

### **Casein kinase II phosphorylation site.**

amino acids 52-56, 95-99, 198-202, 267-271

### **N-myristoylation site.**

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 58

## FIGURE 59

CCCACGCGTCCGCGGACGCGTGGGTGCGACTAGTTCTAGATCGCGAGCGGCCGCCGCGGCTC  
AGGGAGGAGCACCAGCTGCGCCGCACCCTGAGAGATGGTTGGTGCCATGTGGAAGGTGATTG  
TTTCGCTGGTCTGTGATGCCTGGCCCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGT  
GTTTCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTTCTCACCCCTTACATTGAAGC  
TGGGAAGATCCAAAAAGGAAGAGAATTGAGTTTGGTTCGGCCCTTTCCAGGACTGAACATGA  
AGAGTTATGCCGGCTTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTTCTGGTTC  
TTCCCAGCTCAGATACAGCCAGAAGATGCCCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGG  
AGGTTTCATCCATGTTTGGACTCTTTGTGGAACATGGGCCTTATGTTGTCACAAGTAACATGA  
CCTTGCGTGACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTTACATTGACAATCCA  
GTGGGCACAGGCTTCAGTTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGT  
AGCACGGGATTTATACAGTGCCTAATTGAGTTTTCAGATATTTCCCTGAATATAAAAAATA  
ATGACTTTTTATGTCACTGGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC  
ATCCATTCCCTCAACCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA  
TGGATATTCTGATCCCGAATCAATTATAGGGGGCTATGCAGAATTCCTGTACCAAATTGGCT  
TGTTGGATGAGAAGCAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATC  
AGGAAGCAGAAGTGGTTTGGAGCCTTTGAAATACTGGATAAACTACTAGATGGCGACTTAAC  
AAGTGATCCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTTTGCGGT  
GCACGGAACCTGAGGATCAGCTTTACTATGTGAAATTTTTGTCACTCCAGAGGTGAGACAA  
GCCATCCACGTGGGGAATCAGACTTTTAATGATGGAACATAGTTGAAAAGTACTTGCGAGA  
AGATACAGTACAGTCAAGTAAAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGA  
TCTACAATGGCCAACTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGATGGGC  
ATGGACTGGAAAGGATCCAGGAATACAAGAAGGCAGAAAAAAAGTTTGGAAGATCTTTAA  
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTTCCATCAGGTAATTATTC  
GAGGTGGAGGACATATTTTACCCTATGACCAGCCTCTGAGAGCTTTTGACATGATTAATCGA  
TTCATTTATGGAAAAGGATGGGATCCTTATGTTGGATAAACTACCTTCCCAAAGAGAACAT  
CAGAGGTTTTTATTGCTGAAAAGAAAATCGTAAAAACAGAAAATGTCATAGGAATAAAAAAA  
TTATCTTTTCATATCTGCAAGATTTTTTTTCATCAATAAAAAATTATCCTTGAAACAAGTGAGC  
TTTTGTTTTTGGGGGGAGATGTTTACTACAAAATTAACATGAGTACATGAGTAAGAATTACA  
TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAAATGA  
AATTTTAGGGTCTTGAATAGGAAGTTTAAATTTCTTCTAAGAGTAAGTGAAAAGTGCAGTTG  
TAACAAACAAAGCTGTAAACATCTTTTTCTGCCAATAACAGAAGTTTGGCATGCCGTGAAGGT  
GTTTGGAAATATTATTGGATAAGAATAGCTCAATTATCCCAAATAAATGGATGAAGCTATAA  
TAGTTTTGGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAATTCTTTGAAATA  
AAAATATTATATATAAAAGTAAAAA

## **FIGURE 60**

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDGQPLFLTPYIEAGKIQKGRELSL  
VGPFPGNLNPKSYAGFLT VNKTYSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH  
GPYVVTSNMTLRDRDFPWTTL SMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALI QF  
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLI HSLNPVREV KINLNGIAIGDGYSDPESIIGG  
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGDLTSDPSYFQNV TG  
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKPWLT  
EIMNNYKVLIIYNGQLDII VAAALTE RSLMGMDWKGSQEYKKA EKKVWKIFKSDSEVAGYIRO  
AGDFHQV IIRGGGHILPYDQPLRAFD MINRFIYGKGWDPYVG

### **Signal sequence:**

amino acids 1-22

### **N-glycosylation site.**

amino acids 81-85, 132-136, 307-311, 346-350

### **Casein kinase II phosphorylation site.**

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,  
353-357, 424-428

### **Tyrosine kinase phosphorylation site.**

amino acids 423-432

### **N-myristoylation site.**

amino acids 22-28, 110-116, 156-162, 232-238

### **Serine carboxypeptidases, serine active site.**

amino acids 200-208

### **Crystallins beta and gamma 'Greek key' motif signature.**

amino acids 375-391



## FIGURE 61

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGAATCCCAGTCTTGTTGGCTACAACAT  
TTTTCCCTTTCTAACAAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTTCTTCTT  
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTG  
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG  
TCTAAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC  
CTGGGGGAGGGCCTGCCTAACAAGCTTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGAT  
AAGACGTGCCGGTAGGATAGGGAAGACTGGGTTTAGTCCTAATATCAAATTGACTGGCTGGG  
TGAACCTCAACAGCCTTTTAACCTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA  
TAGAGATGCTTTGTAAAATAAAATTTTAAAAAAGCAAGTATTTTATAGCATAAAGGCTAGA  
GACCAAAATAGATAACAGGATTCCCTGAACATTCCTAAGAGGGAGAAAGTATGTTAAAAATA  
GAAAAACCAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGGACCCCTGGGTC  
AGGCCAGCCTCTTTGCTCCTCCCGGAAATTATTTTGGTCTGACCACTCTGCCTTGTGTTTT  
GCAGAATCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT  
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGG  
ACAGCCGCTCTGTGGTCTGCTCTCAGTGGTCTGGGTGCTGCTGGCCCCCAGCAGCCGGC  
ATGCCTCAGTTCAGCACCTTCCACTCTGAGAATCGTGACTGGACCTTCAACCACTTGACCGT  
CCACCAAGGGACGGGGGCCGTCTATGTGGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA  
ACCTGACCATCCAGGTGGCTCATAAGACAGGGGCCAGAAGAGGACAACAAGTCTCGTTACCCG  
CCCCTCATCGTGAGCCCTGCAGCGAAGTGCTCACCTCACCAACAATGTCAACAAGCTGCT  
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGGAGCCTCTACCAGGGGGTCTGCA  
AGCTGCTGCGGCTGGATGACCTTTTCATCCTGGTGGAGCCATCCACAAGAAGGAGCACTAC  
CTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGGTGATTGTGCGCTCTGAGGGTGAGGA  
TGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCCTGTCCA  
GCCGGAAGCTGCCCCGAGACCCTGAGTCTCAGCCATGCTCGACTATGAGCTACACAGCGAT  
TTTGTCTCCTCTCTCATCAAGATCCCTTCAGACACCCTGGCCCTGGTCTCCCACTTTGACAT  
CTTCTACATCTACGGCTTTGCTAGTGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCGAGA  
CCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTTTCTACACCTCACGCATCGTGCGG  
CTCTGCAAGGATGACCCCAAGTTCCACTCATACGTGTCCCTGCCCTTCGGCTGCACCCGGGC  
CGGGGTGGAATACCGCCTCCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCC  
AGGCCTTCAATATCACCAGCCAGGACGATGTACTCTTTGCCATCTTCTCAAAGGGCAGAAG  
CAGTATCACCAACCCGCCGATGACTCTGCCCTGTGTGCCTTCCCTATCCGGGCCATCAACTT  
GCAGATCAAGGAGCGCCTGCAGTCTGCTACCAGGGCGAGGGCAACCTGGAGCTCAACTGGC  
TGCTGGGGAAGGACGTCCAGTGCACGAAGGCGCCTGTCCCATCGATGATAACTTCTGTGGA  
CTGGACATCAACCAGCCCCTGGGAGGCTCAACTCCAGTGGAGGGCCTGACCCTGTACACCAC  
CAGCAGGGACCGCATGACCTCTGTGGCTCCTACGTTTACAACGGCTACAGCGTGGTTTTTG  
TGGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTCAGATGCTCCAATGCC  
ATTACCTCCTCAGCAAAGAGTCCCTCTTGGAAGGTAGCTATTGGTGGAGATTTAACTATAG  
GCAACTTTATTTTCTTGGGGAACAAAGGTGAATGGGGAGGTAAGAAGGGGTAAATTTTGTG  
ACTTAGCTTCTAGCTACTTCTCCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA  
TTTCAATATTTCCCAAACCTTTAAGAAAAAAGCTTTAAGAAGGTACATCTGCAAAAGCAAA

## **FIGURE 62**

MGTLGQASLFAPPGNYFWSHDHSAFCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP  
RALEVDSRSVVLSSVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV  
YKLTGNLTIQVAHKTGPEEDNKSRYPLIVQPCSEVLTLTNNVNKLLIIDYSENRLACGSL  
YQGVCKLLRLDDLFILVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY  
FPTLSSRKLPRDPRESSAMLDYELHSDVSSLIKIPSDTLALVSHFDIFYIYGFASGGFVYFL  
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP  
GDSLAQAFNITSQDDVLFAIFSKGQKQYHHPDDSAFCFAPIRAINLQIKERLQSCYQGEEN  
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG  
YSVVFVGTKSGKLLKVRVYEFRCNSAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

### **Signal sequence:**

amino acids 1-32

### **Transmembrane domain:**

amino acids 71-87

### **N-glycosylation site.**

amino acids 130-134, 145-149, 217-221, 381-385

### **Casein kinase II phosphorylation site.**

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,  
384-388, 471-475, 481-485, 530-534

### **N-myristoylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

Variable	Mean	SD	Min	Max
Age	38.5	12.5	18	65
Gender	0.5	0.5	0	1
Marital Status	0.5	0.5	0	1
Education	12.5	2.5	9	16
Income	35000	15000	10000	70000
Health Status	0.5	0.5	0	1
Exercise Frequency	0.5	0.5	0	1
Stress Level	0.5	0.5	0	1
Sleep Quality	0.5	0.5	0	1
Dietary Habits	0.5	0.5	0	1
Alcohol Consumption	0.5	0.5	0	1
Smoking Status	0.5	0.5	0	1
Family Size	2.5	1.5	1	5
Work Hours	40	10	20	60
Commuting Time	30	15	10	60
Home Ownership	0.5	0.5	0	1
Neighborhood Safety	0.5	0.5	0	1
Access to Healthcare	0.5	0.5	0	1
Community Engagement	0.5	0.5	0	1
Local Economy	0.5	0.5	0	1
Public Services	0.5	0.5	0	1
Environmental Quality	0.5	0.5	0	1
Crime Rate	0.5	0.5	0	1
Infrastructure	0.5	0.5	0	1
Education Quality	0.5	0.5	0	1
Healthcare Access	0.5	0.5	0	1
Job Opportunities	0.5	0.5	0	1
Cost of Living	0.5	0.5	0	1
Quality of Life	0.5	0.5	0	1
Overall Satisfaction	0.5	0.5	0	1

AGGCTCCCGCGCGCGCTGAGTGC GGACTGGAGTGGGAACCCGGGTCCCCGCGCTTAGAGAACACGCGATGACCA  
CGTGGAGCCTCCGCGCGGAGCCGCGCCCGCACGCTGGGACTCCTGCTGCTGGTTCGTTGGGCTTCTGGTGCTCC  
GCAGGCTGGACTGGAGCACCTTGGTCCCTCTGCGGCTCCGCCATCGACAGCTGGGGCTGCAGGCCAAGGGCTGGA  
ACTTCATGCTGGAGGATTCACCTTCTGGATCTTCGGGGGCTCCATCCACTATTTCCGTGTGCCCAGGGAGTACT  
GGAGGGACCGCCTGCTGAAGATGAAGGCCTGTGGCTTGAACACCCCTACCCACCTATGTTCCGTGGACACCTGCATG  
AGCCAGAAAGAGGCAAAATTTGACTTCTCTGGGAACCTGGAGCCTGGAGGCCTTCGTCTGATGGCCGACAGATCG  
GGCTGTGGGTGATTCTGCGTCCAGGCCCTTACATCTCGAGTGAGATGGACCTCGGGGGCTTGCCAGCTGGCTAC  
TCCAAGACCTTGGCATGAGGCTGAGGACAACCTTACAAGGGCTTCACCGAAGCAGTGGAACCTTTATTTTGACCACC  
TGATGTCCAGGGTGGTGCCACTCCAGTACAAGCGTGGGGGACCTATCATTGCCGTGCAGGTGGAGAATGAATATG  
GTTCTCTATAATAAAGACCCCGCATACATGCCCTACGTCAAGAAGGCACTGGAGGACCGTGGCATTGTGGAACTGC  
TCCTGACTTCAGACAACAAGGATGGGCTGAGCAAGGGGATGTTCAGGGGACTCTTGCCACCATCAACTTGCAGT  
CAACACACGAGCTGCAGCTACTTGACCACCTTTCTCTTCAACGCTCCAGGGGACTCAGCCCAAGATGGTGATGGAGT  
ACTGGACGGGTGGTTTGTACTCGTGGGGAGGCCCTACAATATCTTGGATTCTTCTGAGGTTTTGAAAACCGTGT  
CTGCCATTGTGGACGCCGGCTCCTCCATCAACCTCTACATGTTCCACGGAGGCACCAACTTTGGCTTCATGAATG  
GAGCCATGCACCTCCATGACTACAAGTCAGATGTACCAGCTATGACTATGATGCTGTGCTGACAGAAGCCGGCG  
ATTACACGGCCAAGTACATGAAGCTTCGAGACTTCTTCGGCTCCATCTCAGGCATCCCTCTCCCTCCCCACCTG  
ACCTTCTTCCCAAGATGCCGTATGAGCCCTTAACGCCAGTCTTGTACCTGTCTCTGTGGGACGCCCTCAAGTACC  
TGGGGGAGCCCAATCAAGTCTGAAAAGCCCATCAACATGGAGAACCTGCCAGTCAATGGGGGAAATGGACAGTCCCT  
TCGGGTACATTCTCTATGACAGCAGCATACCTCGTCTGGCATCCTCAGTGGCCACGTGCATGATCGGGGGCAGG  
TGTTTGTGAACACAGTATCCATAGGATTCTTGGACTACAAGACAACGAAGATTGCTGTCCCCCTGATCCAGGGTT  
ACACCGTGTCTGAGGATCTTGGTGGAGAATCGTGGGCGAGTCAACTATGGGGAGAATATTGATGACCAGCGCAAAG  
GCTTAATTGAAATCTCTATCTGAATGATTCACCCCTGAAAAACTTCAGAATCTATAGCCTGGATATGAAGAAGA  
GCTTCTTTTCAAGGTTTCGGCTGGACAAATGGNNTTCCCTCCCGAACAACCCACATTACCTGCTTTCTTCTTGG  
GTAGCTTGTCCATCAGCTCCAGCTTGACACCTTTCTGAAGCTGGAGGGCTGGGAGAAGGGGGTGTATTCA  
TCAATGGCCAGAACCTTGGAGCTTACTGGAACATTGGACCCAGAAGACGCTTTACCTCCAGGTCCCTGGTTGA  
GCAGCGGAATCAACCAGGTTCATCGTTTTTGGAGAGCAGATGGCGGGCCCTGCATTACAGTTTACGGAAACCCCC  
ACCTGGGCAGGAACCAGTACATTAAAGTGAAGCGGTGGCACCCCTCCTGCTGGTGCCAGTGGGAGACTGCCGCCCTC  
CTCTTGACCTGAAGCCTGGTGGCTGCTGCCCCACCCCTCACTGCAAAAGCATCTCCTTAAGTAGCAACCTCAGGG  
ACTGGGGGCTACAGTCTGCCCTGTCTCAGCTCAAAACCTTAAGCCTGCAGGGAAGGTTGGATGGCTTGGCG  
TGGCTTTTGTGTGATGATGGCTTTCTTACAGCCCTGCTCTTGTGCGGAGGCTGTGGGCTGTCTCTAGGGTGGGAGC  
AGCTAATCAGATCGCCAGCCTTTTGGCCCTCAGAAAAAGTGCTGAAACGTGCCCTTGCACCCGACGTACAGCCC  
TGCGAGCATCTGCTGGACTCAGGCGTGCTCTTTGCTGGTTCTGGGAGGCTTGGCCACATCCCTCATGGCCCCAT  
TTTATCCCCGAAATCCTGGGTGTGTACCAGTGTAGAGGGTGGGGAAGGGGTGTCTCACCTGAGCTGACTTTGTT  
CTTCTCTTCAACACTTCTTGAGCCTTCTTTGGGATTCTGGAAGGAACCTCGGCGTGAGAAACATGTGACTTCCCCCT  
TCCCTTCCCACCTCGCTGCTTCCCACAGGGTGACAGGCTGGGCTGGAGAAAGCAAATCCTCACCTGCGTCTTCC  
CAAGTTAGCAGGTGTCTCTGGTGTCTCAGTGAGGAGACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCA  
CATCCAGGGAGGAGGACAGAAGGCCCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCC  
AGGGAGGAGGACAGAAGGCCCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGGA  
GGAGGACAGAAGGCCCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGAGGAG  
ACAGAAGTCCCAGCTCAGTGGCCCCGCTCCCCACCCCCACGCCCCAACAGCAGGGGCGAGCAGCCCTCTCTC  
GAAGTGTGTCAGATCCGCAATTTGAGCCTTGTCTGGGGGCCAGCCCAACACCTGGCTTGGGCTCACTGTCTGTA  
GTTGCAAGTAAAGCTATAACCTTGAATCACAA

## **FIGURE 64**

MTTWSLRRRPPARTLGLLLLVLGLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDSTFW  
IFGGSIHVFRVPREYWRDRLLKMKACGLNTLTITYVPWNLHEPERGKFDFSGNLDLEAFVLMA  
AEIGLWVILRPGPYICSEMDLGGPLPSWLLQDPGMLRRTTYKGFTEAVDLYFDHLMSRVVPLQ  
YKRGGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLLTSDNKDGLSKGIVQGVLAT  
INLQSTHELQLLTTFLFNVQGTQPKMVMEYWTGWFDWSGGPHNILDSSSEVLKTVSAIVDAGS  
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTAKYMKLRDFFGSGISGIP  
LPPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSFGYILYE  
TSITSSGILSGHVHDRGQVFVNTVSI GFLDYKTTKIAVPLIQGYTVLRILVENRGRVNYGEN  
IDDQRKGLIGNLYLNDSP LKNFRIYSLDMKKSFFQRFGLDKWXS L PETPTLP AFFLGSL SIS  
STPCDTFLKLEGWEKGVVFINGQNLGRYWNIGPQKTLYLPGPWLSSGINQVIVFEETMAGPA  
LQFTETPHLGRNQYIK

### **Signal sequence:**

amino acids 1-27

### **Casein kinase II phosphorylation site.**

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

### **N-myristoylation site.**

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,  
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

## FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC  
CTGGTGAGGGTTCTCTACTTGGCCTTCGGTGGGGGTCAAGACGCAGGCACCTACGCCAAAGG  
GGAGCAAAGCCGGGCTCGGCCCCGAGGCCCCAGGACCTCCATCTCCCAATGTTGGAGGAATC  
CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC  
AAGAAGCTGTCTGCTTCGTTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCCA  
GGCAGACACTCGGTCGTTTCGTAGTGGATAGGGGTCAATGACCGGTTTTCTCCTAGACGGGGCCC  
CGTTCCGCTATGTGTCTGGCAGCCTGCACTACTTTCGGGTACCGCGGGTGCTTTGGGCCGAC  
CGGCTTTTGAAGATGCGATGGAGCGGCCCTCAACGCCATACAGTTTTATGTGCCCTGGAACCTA  
CCACGAGCCACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGGACCTCATTGCCTTTCTGA  
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTTACATCTGTGCAGAG  
TGGGAGATGGGGGGTCTCCCATCCTGGTTGCTTCGAAAACCTGAAATTCATCTAAGAACCTC  
AGATCCAGACTTCCTTGCCGAGTGGACTCCTGGTTCAAGGTCTTGCTGCCCAAGATATATC  
CATGGCTTTATCACAATGGGGGCAACATCATTAGCATTACAGGTGGAGAATGAATATGGTAGC  
TACAGAGCCTGTGACTTCAGCTACATGAGGCACCTGGCTGGGCTCTTCCGTGCACTGCTAGG  
AGAAAAGATCTTGCTCTTCACCACAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG  
GACTCTATACCACTGTAGATTTTGGCCCAGCTGACAACATGACCAAATCTTTACCCTGCTT  
CGGAAGTATGAACCCCATGGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA  
CTGGGGCCAGAATCACTCCACACGGTCTGTGTGAGCTGTAACCAAAGGACTAGAGAACATGC  
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTTGGATATTGG  
AATGGTGCCGATAAGAAGGGACGCTTCCTTCCGATTACTACCAGCTATGACTATGATGCACC  
TATATCTGAAGCAGGGGACCCACACCTAAGCTTTTTGCTCTTCGAGATGTCATCAGCAAGT  
TCCAGGAAGTTCCTTTGGGACCTTTACCTCCCCGAGCCCCAAGATGATGCTTGGACCTGTG  
ACTCTGCACCTGGTTGGGCATTTACTGGCTTTCCTAGACTTGCTTTGCCCCCGTGGGCCCAT  
TCATTCAATCTTGCCAATGACCTTTGAGGCTGTCAAGCAGGACCATGGCTTCATGTTGTACC  
GAACCTATATGACCCATACCATTTTTTGAGCCAACACCATTTCTGGGTGCCAAATAATGGAGTC  
CATGACCGTGCTATGTGATGGTGGATGGGGTGTTCAGGGTGTGTTGGAGCGAAATATGAG  
AGACAAACTATTTTTGACGGGGAAACTGGGGTCCAAACTGGATATCTTGGTGGAGAACATGG  
GGAGGCTCAGCTTTGGGTCTAACAGCAGTGACTTCAAGGGCCTGTTGAAGCCACCAATTCTG  
GGGCAAACAATCCTTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTTGTGAAGTG  
GTGGTTTCCCCCTCAGTTGCCAAAATGGCCATATCCTCAAGCTCCTTCTGGCCCCACATTCT  
ACTCCAAAACATTTCCAATTTTAGGCTCAGTTGGGGACACATTTCTATATCTACCTGGATGG  
ACCAAGGGCCAAGTCTGGATCAATGGGTTTAACCTGGGCGGTACTGGACAAAGCAGGGGCC  
ACAACAGACCTCTACGTGCCAAGATTCCTGCTGTTTCCCTAGGGGAGCCCTCAACAAAATTA  
CATTGCTGGAACCTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTTTTGGATAAGCCTATC  
CTCAATAGCACTAGTACTTTGCACAGGACACATATCAATTCCCTTTCAGCTGATACACTGAG  
TGCCTCTGAACCAATGGAGTTAAGTGGGCACTGAAAGGTAGGCCGGGCATGGTGGCTCATGC  
CTGTAATCCCAGCACTTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTGAGGACTTCAAGA  
CCAGCCTGGCCAACATGGTGAACCCCGTCTCCACTAAAAATACAAAATTAGCCGGGCGTG  
ATGGTGGGCACCTCTAATCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC  
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTGCACTCCAGCCTGGCTGACAGTGA  
GACACTCCATCTCAAAAAAAAAAAAA

## **FIGURE 66**

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL  
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNNGSRDLIAFLNEAALANLLVILRPGPYI  
CAEWEMGGLPSWLLRKPEIHLRTSDPDLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE  
YGSYRACDFS YMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF  
TLLRKYEYPHGPLVNSEYYTGWLDYWGQNHSTRSVSAVTKGLENMLKLGASVNMVMFHGGTNF  
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLPPSPKMML  
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVPN  
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNS SDFKGLLKP  
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPIILGSVGD TFLYL  
PGWTKGQVWINGFNLGRYWTKQGPQQTLVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD  
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

### **Signal sequence:**

amino acids 1-27

### **N-glycosylation site.**

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 4-8

### **Casein kinase II phosphorylation site.**

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,  
603-607, 644-648

### **Tyrosine kinase phosphorylation site.**

amino acids 191-198

### **N-myristoylation site.**

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,  
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

## FIGURE 67

GCTTTGAACACGTCTGCAAGCCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC  
ACCCACAATATGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT  
TTATGGCTTTATCTGCCTCTACACTCTCTTCTGGTTATTTCAGGATACCTTTGAAGGAATATT  
CTTTCGAAAAAGTCAGAGAAGAGAGCAGTTTTAGTGACATTCCAGATGTCAAAAACGATTTT  
GCGTTCCTTCTTCACATGGTAGAÇCAGTATGACCAGCTATATTCCAAGCGTTTTTGGTGTGTT  
CTTGTGAGAAGTTAGTGAAAATAAACTTAGGGAAATTAGTTTGAACCATGAGTGGACATTTG  
AAAACTCAGGCAGCACATTTTCACGCAACGCCAGGACAAGCAGGAGTTGCATCTGTTTCATG  
CTGTCGGGGGTGCCCGATGCTGTCTTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC  
AATTCAGAAGCTAAAATTCCTGCTAAGATTTCTCAAATGACTAACCTCCAAGAGCTCCACC  
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTTAGCTTTCTTCGCGATCACTTGAGA  
TGCCTTCACGTGAAGTTCACCTGATGTGGCTGAAATTCCTGCCTGGGTGTATTTGCTCAAAAA  
CCTTCGAGAGTTGTACTTAATAGGCAATTTGAACTCTGAAAACAATAAGATGATAGGACTTG  
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCCACGTGAAGAGCAATTTGACCAAAGTT  
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTTCATAATGACGGCAC  
TAAACTCTTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCAGA  
ACTGTGAGCTAGAGAGAATCCACATGCTATTTTCAGCCTCTCTAATTTACAGGAACTGGAT  
TTAAAGTCCAATAACATTCGCACAATTGAGGAAATCATCAGTTTCCAGCATTTAAAACGACT  
GACTTGTTTAAAATTATGGCATAACAAAATTGTTACTATTCTCCCTCTATTACCCATGTCA  
AAAACCTTGAGTCACTTTATTTCTCTAACAACAAGCTCGAATCCTTACCAGTGGCAGTATTT  
AGTTTACAGAACTCAGATGCTTAGATGTGAGCTACAACAACATTTCAATGATTCCAATAGA  
AATAGGATTGCTTCAGAACCTGCAGCATTTGCATATCACTGGGAACAAAGTGGACATTCTGC  
CAAAACAATTGTTTAAATGCATAAAGTTGAGGACTTTGAATCTGGGACAGAACTGCATCACC  
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCCAGCTCACTCAGCTGGAGCTGAAGGGGAAC  
CTTGGACCGCTGCCAGCCCAGCTGGGCCAGTGTCGGATGCTCAAGAAAAGCGGGCTTGTTG  
TGGAAGATCACCTTTTTGATACCCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA  
AATATTCCCTTTGCAAATGGGATTTAAACTAAGATAATATATGCACAGTGATGTGCAGGAAC  
AACTTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTTTAGGAGTAG  
ATACATCTTTTAAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT  
GTTCAATGTTTGTAGGGTTTAAAGTCATTCATTTCCAAATCATTTTTTTTTTTCTTTTGGGG  
AAAGGGAAGGAAAAATTATAATCACTAATCTTGGTTCTTTTTTAAATTGTTTGTAACTTGGAT  
GCTGCCGCTACTGAATGTTTACAAATTGCTTGCCTGCTAAAGTAAATGATTAAATTGACATT  
TTCTTACTAAAAAAAAAAAAAAAAA

Figure 1 consists of 12 sub-graphs labeled (a) through (l), each showing the growth of *E. coli* O157:H7 in ground beef under different conditions. The y-axis for all graphs is  $\log_{10}$  CFU/g, ranging from 0 to 10. The x-axis is time in hours, ranging from 0 to 120. The graphs show various growth curves, including control, heat treatment, and different chemical treatments.

- (a) Control: Shows a steady increase in bacterial count over time, reaching approximately 10  $\log_{10}$  CFU/g by 120 hours.
- (b) Heat treatment: Shows a rapid initial increase in bacterial count, followed by a plateau around 8  $\log_{10}$  CFU/g.
- (c) 10% NaCl: Shows a rapid initial increase in bacterial count, followed by a plateau around 8  $\log_{10}$  CFU/g.
- (d) 10% NaCl + 10% NaOH: Shows a rapid initial increase in bacterial count, followed by a plateau around 8  $\log_{10}$  CFU/g.
- (e) 10% NaCl + 10% NaOH + 10% NaHCO<sub>3</sub>: Shows a rapid initial increase in bacterial count, followed by a plateau around 8  $\log_{10}$  CFU/g.
- (f) 10% NaCl + 10% NaOH + 10% NaHCO<sub>3</sub> + 10% Na<sub>2</sub>CO<sub>3</sub>: Shows a rapid initial increase in bacterial count, followed by a plateau around 8  $\log_{10}$  CFU/g.
- (g) 10% NaCl + 10% NaOH + 10% NaHCO<sub>3</sub> + 10% Na<sub>2</sub>CO<sub>3</sub> + 10% Na<sub>2</sub>SO<sub>4</sub>: Shows a rapid initial increase in bacterial count, followed by a plateau around 8  $\log_{10}$  CFU/g.
- (h) 10% NaCl + 10% NaOH + 10% NaHCO<sub>3</sub> + 10% Na<sub>2</sub>CO<sub>3</sub> + 10% Na<sub>2</sub>SO<sub>4</sub> + 10% Na<sub>2</sub>PO<sub>4</sub>: Shows a rapid initial increase in bacterial count, followed by a plateau around 8  $\log_{10}$  CFU/g.
- (i) 10% NaCl + 10% NaOH + 10% NaHCO<sub>3</sub> + 10% Na<sub>2</sub>CO<sub>3</sub> + 10% Na<sub>2</sub>SO<sub>4</sub> + 10% Na<sub>2</sub>PO<sub>4</sub> + 10% Na<sub>2</sub>SiO<sub>3</sub>: Shows a rapid initial increase in bacterial count, followed by a plateau around 8  $\log_{10}$  CFU/g.
- (j) 10% NaCl + 10% NaOH + 10% NaHCO<sub>3</sub> + 10% Na<sub>2</sub>CO<sub>3</sub> + 10% Na<sub>2</sub>SO<sub>4</sub> + 10% Na<sub>2</sub>PO<sub>4</sub> + 10% Na<sub>2</sub>SiO<sub>3</sub> + 10% Na<sub>2</sub>Al<sub>2</sub>Si<sub>2</sub>O<sub>8</sub>: Shows a rapid initial increase in bacterial count, followed by a plateau around 8  $\log_{10}$  CFU/g.
- (k) 10% NaCl + 10% NaOH + 10% NaHCO<sub>3</sub> + 10% Na<sub>2</sub>CO<sub>3</sub> + 10% Na<sub>2</sub>SO<sub>4</sub> + 10% Na<sub>2</sub>PO<sub>4</sub> + 10% Na<sub>2</sub>SiO<sub>3</sub> + 10% Na<sub>2</sub>Al<sub>2</sub>Si<sub>2</sub>O<sub>8</sub> + 10% Na<sub>2</sub>Fe<sub>2</sub>(SO<sub>4</sub>)<sub>6</sub>: Shows a rapid initial increase in bacterial count, followed by a plateau around 8  $\log_{10}$  CFU/g.
- (l) 10% NaCl + 10% NaOH + 10% NaHCO<sub>3</sub> + 10% Na<sub>2</sub>CO<sub>3</sub> + 10% Na<sub>2</sub>SO<sub>4</sub> + 10% Na<sub>2</sub>PO<sub>4</sub> + 10% Na<sub>2</sub>SiO<sub>3</sub> + 10% Na<sub>2</sub>Al<sub>2</sub>Si<sub>2</sub>O<sub>8</sub> + 10% Na<sub>2</sub>Fe<sub>2</sub>(SO<sub>4</sub>)<sub>6</sub> + 10% Na<sub>2</sub>Fe<sub>2</sub>(SO<sub>4</sub>)<sub>6</sub>: Shows a rapid initial increase in bacterial count, followed by a plateau around 8  $\log_{10}$  CFU/g.

Signal sequence:

N-glycosylation site.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

**Tyrosine kinase phosphorylation site.**

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398



## FIGURE 69

CCCACGCGTCCGGCCTTCTCTCTGGACTTTGCATTTCCATTCCCTTTTCATTGACAAACTGACTTTTTTTTATTTCT  
TTTTTTCCATCTCTGGGCCAGCTTGGGATCCTAGGCCGCCCTGGGAAGACATTTGTGTTTTACACACATAAGGAT  
CTGTGTTTTGGGGTTTTCTTCTTCCCTCCCTGACATTGGCATTTGCTTAGTGTTTGTGTGGGGAGGGAGACCACGTGG  
GCTCAGTGTCTTGTCTGCACTTATCTGCTAGGTACATCGAAGTCTTTTGACCTCCATACAGTGATTATGCCTGTC  
ATCGCTGGTGGTATCCTGGCGGCCCTTGTCTGTGATAGTTGTCTGTCTTACTTCAAAATACACAAC  
GCGCTAAAAGCTGCAAAGGAACCTGAAGCTGTGGCTGTAAAAAATCACAACCCAGACAAGGTGTGGTGGGCCAAG  
AACAGCCAGGCCAAAACCATTTGCCACGGAGTCTTGTCTGCTGCCCTGCAGTGTGTGAAGGATATAGAATGTGTGCC  
AGTTTTGATTTCCCTGCCACCTTGTCTGTGCGACATAAATGAGGGCCTCTGAGTTAGGAAAGGCTCCCTTCTCAA  
GCAGAGCCCTGAAGACTTCAATGATGTCAATGAGGCCACCTGTTTGTGATGTGCAGGCACAGAAGAAAGGCACAG  
CTCCCCATCAGTTTTCATGGAAAATAACTCAGTGCCTGTCTGGGAACCAGCTGTCTGGAGATCCCTACAGAGAGCTTC  
CACTGGGGGCAACCTTCCAGGAAGGAGTTGGGGAGAGAGAACCCTCACTGTGGGGAATGCTGATAAACAGTCA  
CACAGCTGCTCTATTCTCACACAAATCTACCCCTTGCCTGGCTGGAACTGACGTTTCCCTGGAGGTGTCCAGAAA  
GCTGATGTAACACAGAGCCTATAAAAGCTGTCTGGTCTTTAAGGCTGCCAGCGCCTTGCCAAAATGGAGCTTGTA  
AGAAGGCTCATGCCATTGACCCCTCTTAATTTCTCTCTGTTTGGCGGAGCTGACAATGGCGGAGGCTGAAGGCAAT  
GCAAGCTGCACAGTCACTTAGGGGGTGCCAATATGGCAGAGACCCACAAAGCCATGATCCTGCAACTCAATCCC  
AGTGAGAACTGCACCTGGACAATAGAAAAGACCAGAAAAACAAAAGCATCAGAATTATCTTTTCTATGTCCAGCTT  
GATCCAGATGGAAGCTGTGAAAGTGAAGACATTAAGTCTTTGACGGAACCTCCAGCAATGGGCCTCTGCTAGGG  
CAAGTCTGCAGTAAAAACGACTATGTTCTGTATTTGAATCATCTCAGTACATTGACGTTTCAAATAGTTACT  
GACTCAGCAAGAATTCAAAGAAGTGTCTTTGTCTTCTACTACTTCTTCTCTCTTAACATCTCTATTCCAAACTGT  
GGCGGTTACCTGGATACCTTGGGAAGGATCCCTCACCAGCCCCAATTACCCAAAGCCGCATCCTGAGCTGGCTTAT  
TGTGTGTGGCACATACAAGTGGAGAAAGATTACAAGATAAACTAAACTTCAAAGAGATTTTCTTAGAAAATAGAC  
AAACAGTGCAAATTTGATTTTCTTGCCATCTATGATGGCCCCCTCCACCAACTCTGGCCTGATTGGACAAGTCTGT  
GGCCGTGTGACTCCCACCTTGAATCGTCACTCAAACTCTCTGACTGTCTGTGTGTCTACAGATTATGCCAATTCT  
TACCGGGGATTTTCTGCTTCTTACACCTCAATTTATGCAGAAAACATCAACACTACATCTTTAACTTGCTCTTCT  
GACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGCTTTTAACTCTAATGGGAATAACTTGCAACTAAAA  
GACCCAACTTGACAGACCAAAATTTATCAAATGTTGTGGAATTTTCTGTCCCTCTTAATGGATGTGGTACAATCAGA  
AAGGTAGAAGATCAGTCAATTTACTTACACCAATATAATCACCTTTTCTGCATCCTCAACTTCTGAAGTGATCACC  
CGTCAGAAAACACTCCAGATTATTGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATACATAACA  
GAAGATGATGTAATACAAAGTCAAAATGCACTGGGCAATATAACACCAGCATGGCTCTTTTGAATCCAATTCA  
TTTGAAGAACTATACTTGAATCACCATATTATGTGGATTTGAACCAACTCTTTTGTTCAGTTAGTCTGCAC  
ACCTCAGATCCAAATTTGGTGGTGTCTTGTGATACCTGTAGAGCCTCTCCACCTCTGACTTTGCATCTCCAACC  
TACGACCTAATCAAGAGTGGATGTAGTCGAGATGAACTTGTAAAGGTGTATCCCTTATTTGGACACTATGGGAGA  
TTCCAGTTTAAATGCCCTTTAAATTTCTTGAGAAGTATGAGCTCTGTGTATCTGCAGTGTAAAGTTTGGATATGTGAT  
AGCAGTGACCACAGTCTCGCTGCAATCAAGGTTGTGTCTCCAGAAGCAAACGAGACATTTCTTCATATAAAATGG  
AAAACAGATTCCATCATAGGACCCATTCGTCTGAAAAGGGATCGAAGTGCAAGTGGCAATTCAGGATTTACAGAT  
GAAACACATGCGGAAGAACTCCAAACCAGCCTTTCAACAGTGTGCATCTGTTTTCTTCAATGGTTCTAGCTCTG  
AATGTGGTGAAGTGTAGCGACAATCACAGTGAGGCATTTTGTAAATCAACGGGCAGACTACAAATACCAGAAGCTG  
CAGAACTATTAACTAACAGGTCCAACCCTAAGTGAGACATGTTTCTCCAGGATGCCAAAGGAAATGCTACCTCGT  
GGCTACACATATTATGAATAAATGAGGAAGGGCTGAAAGTGACACACAGGCCTGCATGTAAAAAAA

## **FIGURE 70**

MELVRRRLMPLTLLILSCLAELTMAEAEAGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI  
ERPENKSIRIIFSIVQLDPDGSCSENIKVFDGTSSNGPLLQVCSKNDYVPVFESSSSTLT  
FQIVTDSARIQRTVFVFFYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV  
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCGRVTPTFESSSNSLTVVLS  
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVVISKSYLEAFNSNGNNLQLKDPTCRP  
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQQLQIIVKCEMGNST  
VEIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPN  
LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSVYL  
QCKVLICDSSDHQSRCNQGCVSRSKRDISSYKWKTDIIGPIRLKRDRSASGNSGFQHETHA  
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

### **Signal sequence:**

amino acids 1-24

### **Transmembrane domain:**

amino acids 571-586

### **N-glycosylation site.**

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,  
394-398, 419-423

### **Casein kinase II phosphorylation site.**

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,  
408-412, 463-467, 520-524, 556-560

### **Tyrosine kinase phosphorylation site.**

amino acids 172-180, 407-415, 407-416, 519-528

### **N-myristoylation site.**

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG  
GGACATGCGGCCCCAGGAGCTCCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGTTGCTGC  
TGCTGCCGCCGCCGCGCTGCCCTGCCACAGCGCCACGCGCTTCGACCCACCTGGGAGTCC  
CTGGACGCCCCGCGAGCTGCCCGCGTGGTTTGACCAGGCCAAGTTCGGCATCTTCATCCACTG  
GGGAGTGTTCCTCGTGCCAGCTTCGGTAGCGAGTGGTTCCTGGTGGTATTGGCAAAAGGAAA  
AGATACCGAAGTATGTGGAATTTATGAAAGATAATTACCCTCCTAGTTTCAAATATGAAGAT  
TTTGGACCACTATTTACAGCAAAATTTTTTAATGCCAACCAGTGGGCAGATATTTTTTCAGGC  
CTCTGGTGCCAAATACATTGTCTTAACTTCCAAACATCATGAAGGCTTTACCTTGTGGGGGT  
CAGAATATTCGTGGAACCTGGAATGCCATAGATGAGGGGGCCCAAGAGGGACATTGTCAAGGAA  
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTTTTGGACTGTACTATTCCCTTTTTGA  
ATGGTTTTCATCCGCTCTTCCTTGAGGATGAATCCAGTTCATTCCATAAGCGGCAATTTCCAG  
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATATCAGCCTGAGGTTCTGTGG  
TCGGATGGTGACGGAGGAGCACCGGATCAATACTGGAACAGCACAGGCTTCTTGGCCTGGTT  
ATATAATGAAAGCCAGTTCGGGGCACAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCA  
TCTGTAAGCATGGTGGCTTCTATACCTGCAGTGATCGTTATAACCCAGGACATCTTTTGCCA  
CATAAATGGGAAAACCTGCATGACAATAGACAAACTGTCCTGGGGCTATAGGAGGGAAGCTGG  
AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTTCATGTG  
GAGGAAATCTTTTGATGAATATTGGGCCCCACACTAGATGGCACCATTTCTGTAGTTTTTGAG  
GAGCGACTGAGGCAAGTGGGGTCTGGCTAAAAGTCAATGGAGAAGCTATTTATGAAACCTA  
TACCTGGCGATCCCAGAATGACACTGTCACCCAGATGTGTGGTACACATCCAAGCCTAAAG  
AAAAATTAGTCTATGCCATTTTTCTTAAATGGCCACATCAGGACAGCTGTTCCCTTGCCAT  
CCCAAAGCTATTCTGGGGGCAACAGAGGTGAACTACTGGGCCATGGACAGCCACTTAACTG  
GATTTCTTTGGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTATCAGATGC  
CGTGTAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATCTTAAAGTGCAGCAGAGTGGCTG  
ATGCTGCAAGTTATGTCTAAGGCTAGGAACTATCAGGTGTCTATAATTGTAGCACATGGAGA  
AAGCAATGTAACTGGATAAGAAAATTATTTGGCAGTTCAGCCCTTTCCCTTTTTCCCACTA  
AATTTTTCTTAAATTACCCATGTAACCATTTTAACTCTCCAGTGCACCTTTGCCATTAAAGTC  
TCTTCACATTGATTTGTTTCCATGTGTGACTCAGAGGTGAGAATTTTTTTCACATTATAGTAG  
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTTTATGTTGAAGCCATATCCCCCATG  
ATTATATAGTTATGCATCACTTAATATGGGGATATTTCTGGGAAATGCATTGCTAGTCAAT  
TTTTTTTTTGTGCCAACATCATAGAGTGTATTTACAAAATCCTAGATGGCATAGCCTACTACA  
CACCTAATGTGTATGGTATAGACTGTTGCTCCTAGGCTACAGACATATACAGCATGTTACTG  
AATACTGTAGGCAATAGTAACAGTGGTATTTGTATATCGAAACATATGGAAACATAGAGAAG  
GTACAGTAAAAATACTGTAAAATAAATGGTGCACCTGTATAGGGCACTTACCACGAATGGAG  
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA  
TTGAACACTGCCAGACGTTATAAATACTGTATGCTTAGGCTACACTACATTTATAAAAAAAA  
GTTTTTCTTTCTTCAATTATAAATTAACATAAGTGTACTGTAACCTTACAAACGTTTTAATT  
TTTAAAACCTTTTTTGGCTCTTTTGTAATAACACTTAGCTTAAAACATAAACTCATTGTGCAA  
ATGTAA

## **FIGURE 72**

MRPQELPRLAFPLLLLLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHWG  
VFSVPSEFGSEWFWWYWQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWADIFQAS  
GAKYIVLTSTKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRFGLYYSLFEW  
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWNSTGFLAWLY  
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI  
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT  
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI  
SLEQNGIMVELPQLTIHQMPCKKGWALALTNVI

### **Signal sequence:**

amino acids 1-28

### **N-glycosylation site.**

amino acids 171-175, 239-243, 377-381

### **Casein kinase II phosphorylation site.**

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,  
375-375

### **Tyrosine kinase phosphorylation site.**

amino acids 361-369, 389-397

### **N-myristoylation site.**

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

### **Leucine zipper pattern.**

amino acids 410-432

### **Alpha-L-fucosidase putative active site.**

amino acids 283-295

## FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT  
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATC  
TGAGGTGTTTTCCCTGGCTCTGAAGGGGTAGGCACGATGCGCCAGGTGCTTCAGCCTGGTGTG  
CTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCT  
TTCCATCCAGGTGTCATGCAGAATTATGGGGATCACCTTGTGAGCAAAAAGGCGAACCAGC  
AGCTGAATTTACAGAAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAG  
GACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGA  
TGGATTCTGGTTCATCTCTAGGATTAGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTG  
TCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGAT  
ACTTGGACTAACTCGTGCATTCCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCA  
AACTGCAACACAAACAACAGAATTTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCCTT  
ACTCTACAATACCTGCCCCCTACTACTCTCCTGCTCCAGCTTCCACTTCTATTCCACGG  
AGAAAAAAATTGATTTGTGTACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAAC  
TGAACCATTTGTTGAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCC  
CCACGGCTCTGCTAGTGCTTGTCTCTCCTCTTCTTTGGTGTGCTGCAGCTGGTCTTGGATTTTGC  
TATGTCAAAGGTATGTGAAGGCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGAT  
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGA  
AAACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACTACCGTGCGATGCCTGGAA  
GCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCC  
TTACCCTGCCCCAGCTGGGGAAATCAAAGGGCCAAAGAACCAAAGAAGAAAGTCCACCCTT  
GGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGC  
CCTTCTCCTTATTGTAACCCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCC  
TTTCTAGCCTGGCTATGTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTTGCAAAGTGCAA  
GGACCTAAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGG  
TGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCGCAGCTCAGAC  
CCTTTCTTCAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCTTCTGAGCCCGGTA  
AGAGCAAAAGAATGGCAGAAAAGTTTAGCCCCCTGAAAGCCATGGAGATTCTCATAACTTGAG  
ACCTAATCTCTGTAAAGCTAAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTAACT  
GTCAGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGA  
ATCACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT  
AGGAAATATACTTTTACAAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTTTATCTGA  
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATTCA  
ACAAACATTTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTCTGTAAT  
TGAATATTATTCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTTTTTTCA  
GTTTTGATATTTCTAGCTTATCTACTTCCAACTAATTTTTTATTTTTGCTGAGACTAATCTT  
ATTCATTTTCTCTAATATGGCAACCATTATAACCTTAATTTATTATTAACATACCTAAGAAG  
TACATTGTTACCTCTATATAACCAAGCACATTTTAAAAGTGCCATTACAAATGTATCACTA  
GCCCTCCTTTTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTTGTGACAAAAAATTAA  
AGCATTTAGAAAACCTT

## **FIGURE 74**

MARCFSLVLLLLTSIWTTTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR  
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLWKVPVSRQF  
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP  
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFF  
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPPEESKSP  
SKTTVRCLEAEV

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 235-254

### **N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

### **Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

### **Tyrosine kinase phosphorylation site.**

amino acids 79-88

### **N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

Figure 1 consists of 12 scatter plots, labeled (a) through (l), each showing the relationship between a specific variable and the number of children. The variables are: (a) Age, (b) Sex, (c) Education, (d) Income, (e) Religion, (f) Ethnicity, (g) Marital status, (h) Employment, (i) Health, (j) Social capital, (k) Parental involvement, and (l) Parental satisfaction. Each plot shows a different trend, with some showing a positive correlation and others a negative correlation.

1

## **FIGURE 76**

MAVLAPLIALVYSVPRLSRWLAQPYLLSALLSAAFLLRKLPPLCHGLPTQREDGNPCDFD  
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL  
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPITYADLSLKYNC  
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE  
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

### **Signal sequence:**

amino acids 1-48

### **Transmembrane domain:**

amino acids 111-125

### **N-glycosylation site.**

amino acids 165-169, 185-189

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 154-158, 265-269

### **Casein kinase II phosphorylation site.**

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

### **N-myristoylation site.**

amino acids 188-194, 225-231

### **Myb DNA-binding domain repeat signature 1.**

amino acids 244-253



## FIGURE 77

GGACAGCTCGCGGCCCCGAGAGCTCTAGCCGTCGAGGAGCTGCCTGGGGACGTTTGCCCTG  
GGGCCCCAGCCTGGCCCGGGTCACCCTGGCATGAGGAGATGGGCCTGTTGCTCCTGGTCCCA  
TTGCTCCTGCTGCCCCGGCTCCTACGGACTGCCCTTCTACAACGGCTTCTACTACTCCAACAG  
CGCCAACGACCAGAACCTAGGCAACGGTCATGGCAAAGACCTCCTTAATGGAGTGAAGCTGG  
TGTTGGAGACACCCGAGGAGACCCTGTTACCTACCAAGGGGCCAGTGTGATCCTGCCCTGC  
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCCGCGGCGTGTGCGTGTCAAATGGTGGAAGCT  
GTCGGAGAACGGGGCCCCAGAGAAGGACGTGCTGGTGGCCATCGGGCTGAGGCACCGCTCCT  
TTGGGGACTACCAAGGCCGCGTGCACCTGCGGCAGGACAAAGAGCATGACGTCTCGCTGGAG  
ATCCAGGATCTGCGGCTGGAGGACTATGGGCGTTACCGCTGTGAGGTCATTGACGGGCTGGA  
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCGGGGTGTGGTCTTTCCTTACCAGTCCCCCA  
ACGGGCGCTACCAGTTCAACTTCCACGAGGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCGGCTG  
GTGGCCTCCTTTGAGCAGCTCTTCCGGGCTGGGAGGAGGGCCTGGACTGGTGCAACGCGGG  
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCCGGCAGCCCTGCGGTGGCC  
CAGGCCTGGCACCTGGCGTGCGAAGCTACGGCCCCCGCCACCGCCGCTGCACCGCTATGAT  
GTATTCTGCTTCGCTACTGCCCTCAAGGGGCGGTGTACTACCTGGAGCACCTGAGAAGCT  
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATCGCCAAGGTGGGAC  
AGCTCTTTGCCGCCTGGAAGTTCATGGCCTGGACCGCTGCGACGCTGGCTGGCTGGCAGAT  
GGCAGCGTCCGCTACCCTGTGGTTCACCCGCATCCTAACTGTGGGCCCCCAGAGCCTGGGGT  
CCGAAGCTTTGGCTTCCCCGACCCGCAGAGCCGCTTGTACGGTGTTTACTGCTACCGCCAGC  
ACTAGGACCTGGGGCCCTCCCCTGCCGCATTCCCTCACTGGCTGTGTATTTATTGAGTGGTT  
CGTTTTTCCCTTGTGGGTGGAGCCATTTTAACTGTTTTTATACTTCTCAATTTAAATTTTCT  
TTAAACATTTTTTTTACTATTTTTTTGTAAAGCAAACAGAACCCAATGCCTCCCTTTGCTCCTG  
GATGCCCCACTCCAGGAATCATGCTTGCTCCCCTGGGCCATTTGCGGTTTTTGTGGGCTTCTG  
GAGGGTTCCCCGCCATCCAGGCTGGTCTCCCTCCCTTAAGGAGGTTGGTGCCAGAGTGGGC  
GGTGGCCTGTCTAGAATGCCGCCGGGAGTCCGGGCATGGTGGGCACAGTTCTCCCTGCCCCT  
CAGCCTGGGGGAAGAAGAGGGCCTCGGGGGCCTCCGGAGCTGGGCTTTGGGCCTCTCCTGCC  
CACCTCTACTTCTCTGTGAAGCCGCTGACCCAGTCTGCCCACTGAGGGGCTAGGGCTGGAA  
GCCAGTTCTAGGCTTCCAGGCGAAATCTGAGGGAAGGAAGAACTCCCCCTCCCCGTTCCCTT  
TCCCCTCTCGGTTCCAAAGAATCTGTTTTTGTGTGTCATTTGTTTTCTCCTGTTTTCCCTGTGTGG  
GGAGGGGCCCTCAGGTGTGTGTACTTTGGACAATAAATGGTGCTATGACTGCCTTCCGCCAA  
AA  
AA

## **FIGURE 78**

MGLLLLVPLLLLPGSYGLPFYNGFYYSNSANDQNLGNGHGKDLLNGVKLVVETPEETLFTYQ  
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD  
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ  
VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR  
HRR LHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR  
CDAGWLADGSVRYFPVVHPPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

### **Signal sequence:**

amino acids 1-17

### **Casein kinase II phosphorylation site.**

amino acids 29-33, 53-57, 111-115, 278-282

### **Tyrosine kinase phosphorylation site.**

amino acids 137-145

### **N-myristoylation site.**

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

## FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCGATGATGTGGCGACCATCAGTTCTGCTGC  
TTCTGTTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC  
CAGGGGAGGGTGCACCAGGCGGGCCCCCTGAGCGACGCTCCCCATGATGACGCCACGGGAA  
CTTCCAGTACGACCATGAGGCTTTCTCTGGGACGGGAAGTGGCCAAGGAATTCGACCAACTCA  
CCCCAGAGGAAAGCCAGGCCCGTCTGGGGCGGATCGTGGACCGCATGGACCGCGCGGGGGAC  
GGCGACGGCTGGGTGTCGCTGGCCGAGCTTCGCGCGTGGATCGCGCACACGCAGCAGCGGCA  
CATACGGGACTCGGTGAGCGCGGCCTGGGACACGTACGACACGGACCGCGACGGGCGTGTGG  
GTTGGGAGGAGCTGCGCAACGCCACCTATGGCCACTACGCGCCCGGTGAAGAATTTTCATGAC  
GTGGAGGATGCAGAGACCTACAAAAGATGCTGGCTCGGGACGAGCGGCGTTTCCGGGTGGC  
CGACCAGGATGGGGACTCGATGGCCACTCGAGAGGAGCTGACAGCCTTCCTGCACCCCGAGG  
AGTTCCCTCACATGCGGGACATCGTGATTGCTGAAACCCTGGAGGACCTGGACAGAAACAAA  
GATGGCTATGTCCAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGGAGGA  
GGAGCCGGCGTGGGTGCAGACGGAGAGGCAGCAGTTCCGGGACTTCCGGGATCTGAACAAGG  
ATGGGCACCTGGATGGGAGTGAGGTGGGCCACTGGGTGCTGCCCCCTGCCCAGGACCAGCCC  
CTGGTGGAAGCCAACCACCTGCTGCACGAGAGCGACACGGACAAGGATGGGCGGCTGAGCAA  
AGCGGAAATCCTGGGTAATTGGAACATGTTTGTGGGCAGTCAGGCCACCAACTATGGCGAGG  
ACCTGACCCGGCACCACGATGAGCTGTGAGCACC CGCACCTGCCACAGCCTCAGAGGCCCCG  
CACAATGACCGGAGGAGGGGCCGCTGTGGTCTGGCCCCCTCCCTGTCCAGGCCCCGCAGGAG  
GCAGATGCAGTCCCAGGCATCCTCCTGCCCCCTGGGCTCTCAGGGACCCCCTGGGTGCGCTTC  
TGTCCCTGTACACCCCCAACCCAGGGAGGGGCTGTCATAGTCCCAGAGGATAAGCAATAC  
CTATTTCTGACTGAGTCTCCAGCCCAGACCCAGGGACCCTTGGCCCCAAGCTCAGCTCTAA  
GAACCGCCCCAACCCCTCCAGCTCCAAATCTGAGCCTCCACCACATAGACTGAAACTCCCCCT  
GGCCCCAGCCCTCTCCTGCCTGGCCTGGCCTGGGACACCTCCTCTCTGCCAGGAGGCAATAA  
AAGCCAGCGCCGGGACCTTGAAA  
AAAAAAAAAAAAAAAAA

## **FIGURE 80**

MMWRPSVLLLLLLLLLRHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR  
EVAKEFDQLTPPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT  
YDTDRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE  
ELTAFLHPPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPWVQTERQQ  
FRDFRDLNKDGHLDGSEVGHVWLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV  
GSQATNYGEDLTRHHDEL

### **Signal sequence:**

amino acids 1-20

### **N-glycosylation site.**

amino acids 140-144

### **Casein kinase II phosphorylation site.**

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,  
291-295, 298-302

### **N-myristoylation site.**

amino acids 263-269, 311-317

### **Endoplasmic reticulum targeting sequence.**

amino acids 325-330

090455-07140  
104720-95610660

## FIGURE 81

GGGGCCTTGCCTTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG  
GCGGCGGGCGCGGGTGCGAGGGATCCCTGACGCCTCTGTCCCTGTTTCTTTGTGCTCCCG  
CCTGTCTGTCTGTCGTTTGGCGCCCCCGCCTCCCCGCGGTGCGGGGTTCACACCGGATCCTG  
GGCTTCGCTCGATTTGCCGCGGAGGCGCCTCCAGACCTAGAGGGGCGCTGGCCTGGAGCAG  
CGGGTCGTCTGTCTCTCTCTCTCTGCGCGCGCGCCGGGGATCCGAAGGGTGCGGGGCTCT  
GAGGAGGTGACGCGCGGGGCCCTCCCGCACCTTGGCCTTGCCCGCATCTCTCCCTCTCTCCAG  
GTGTGAGCAGCCTATCAGTCACCATGTCCGAGCCTGGATCCCGGCTCTCGGCCTCGGTGTG  
TGTCTGCTGCTGCTGCCGGGGCCCCGCGGGCAGCGAGGGAGCCGCTCCCATTTGCTATCACATG  
TTTTACCAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCCGGGGGCTGCC  
CTCTTGAGGAATTCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG  
GCTGCTGTCCACAGGGGAGTAATCAGCAACTCAGGGGGACCTGTACGAGTCTATAGCCTACC  
TGGTCGAGAAAACCTATTCCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTTCTAGAT  
GGTCTGCTTCTTTCACAGTAACTAAAGGCCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA  
GTGTCCACAGCACATCCACCAACAGGTAACGACTAAAGAAAACACCCGAGAAGAAAACCTGG  
CAATAAAGATTGTAAAGCAGACATTGCATTTCTGATTGATGGAAGCTTTAATATTGGGCAGC  
GCCGATTTAATTTACAGAAGAATTTTGTGGAAAAGTGGCTCTAATGTTGGGAATTGGAACA  
GAAGGACCACATGTGGGCCTTGTTCAGCCAGTGAACATCCCAAATAGAATTTTACTTGAA  
AACTTTACATCAGCCAAAGATGTTTTGTTTGCCATAAAGGAAGTAGGTTTCAGAGGGGGTA  
ATTCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATTCTTCACGGTAGATGCTGGA  
GTAAGAAAAGGGATCCCCAAAGTGGTGGTGGTATTTATTGATGGTTGGCCTTCTGATGACAT  
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCTGTGGCCA  
AGCCTATCCCTGAAGAACTGGGGATGGTTCAGGATGTACATTTGTTGACAAGGCTGTCTGT  
CGGAATAATGGCTTCTTCTCTTACCACATGCCCAACTGGTTTGGCACCACAAAATACGTAAA  
GCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCAGCAAGACCTGTTATAACT  
CAGTGAACATTGCCTTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTTCCGCCTC  
ATGCTTGAATTTGTTTCCAACATAGCCAAGACTTTTGAAATCTCGGACATTGGTGCCAAGAT  
AGCTGCTGTACAGTTTACTTATGATCAGCGCACGGAGTTCAGTTTCACTGACTATAGCACCA  
AAGAGAATGTCCTAGCTGTCTATCAGAAACATCCGCTATATGAGTGGTGGAACAGCTACTGGT  
GATGCCATTTCTTCACTGTTAGAAATGTGTTTGGCCCTATAAGGGAGAGCCCCAACAAAGAA  
CTTCCTAGTAATTGTCACAGATGGGCAGTCCATGATGATGTCCAAGGCCCTGCAGCTGCTG  
CACATGATGCAGGAATCACTATCTTCTCTGTTGGTGTGGCTTGGGCACCTCTGGATGACCTG  
AAAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTTCTTCACAAGAGAGTTCACAGGATT  
AGAACCAATTGTTTCTGATGTCTATCAGAGGCATTGTAGAGATTCTTAGAATCCCAGCAAT  
AATGGTAACATTTTGACAACTGAAAGAAAAAGTACAAGGGGATCCAGTGTGTAAATTGTATT  
CTCATAATACTGAAATGCTTTAGCATACTAGAATCAGATACAAAACCTATTAAGTATGTCAAC  
AGCCATTTAGGCAAATAAGCACTCCTTTAAAGCCGCTGCCTTCTGGTTACAATTTACAGTGT  
ACTTTGTTAAAAACACTGCTGAGGCTTCATAATCATGGCTCTTAGAAACTCAGGAAAGAGGA  
GATAATGTGGATTAAAACCTTAAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAAA  
TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAAAAAAAAAA

## **FIGURE 82**

MSAAWIPALGLGVCLLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPPGGCPLEEFVY  
GNIVYASVSSICGAAVHRGVI SNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT  
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKN  
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAlKEVGFRGGNSNTGKAL  
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG  
MVQDVTTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI  
DGSSSVGDSNFRMLLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI  
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAAHDAGITI  
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

### **Signal sequence:**

amino acids 1-24

### **N-glycosylation site.**

amino acids 100-104, 221-225

### **Casein kinase II phosphorylation site.**

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,  
425-429, 478-482, 528-532

### **N-myristoylation site.**

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,  
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

### **Amidation site.**

amino acids 145-149

## FIGURE 83

CGCCGCGCTCCCGCACCCGCGGCGCCGCCCACCGCGCCGCTCCCGCATCTGCACCCGCAGCCC  
GGCGGCCTCCCGGCGGGAGCGAGCAGATCCAGTCCGGCGCCGCGAGCGCAACTCGGTCCAGTCG  
GGGCGGCGGCTGCGGGCGCAGAGCGGAGATGCGAGCGGCTTGGGGCCACCCTGCTGTGCCTGC  
TGCTGGCGGCGGCGGTCCCCACGGCCCCCGCGCCGCTCCGACGGCGACCTCGGCTCCAGTC  
AAGCCCCGGCCCGGCTCTCAGCTACCCGCAGGAGGAGGCCACCCTCAATGAGATGTTCCGCGA  
GGTTGAGGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCCAGCTAT  
CACAAATGAGACCAACACAGACACGAAGGTTGGAAATAATACCATCCATGTGCACCGAGAAAT  
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTTCAGAGACAGTTATCACATCTG  
TGGGAGACGAAGAAGGCAGAAGGAGCCACGAGTGCATCATCGACGAGGACTGTGGGCCCAGC  
ATGTACTGCCAGTTTGGCAGCTTCCAGTACACCTGCCAGCCATGCCGGGGCCAGAGGATGCT  
CTGCACCCGGGACAGTGAGTGCTGTGGAGACCAGCTGTGTGTCTGGGGTCACTGCACCAAAA  
TGGCCACCAGGGGCAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGGCTG  
TGCTGTGCCTTCCAGAGAGGGCCTGCTGTTCCCTGTGTGCACACCCCTGCCCGTGGAGGGCGA  
GCTTTGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCACCTGGGAGCTAGAGCCTGATG  
GAGCCTTGGACCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGCCCCACAGCCACAGCCTG  
GTGTATGTGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGGGAGATCCTGCTGCC  
CAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCGCCAGGAGCTGG  
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCGGCTGCCGCCGCT  
GCACTGCTGGGAGGGGAAGAGATTAGATCTGGACCAGGCTGTGGGTAGATGTGCAATAGAA  
ATAGCTAATTTATTTCCCCAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCTTACA  
TCTTCTTCCCAGTAAGTTTCCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTTGTTTCA  
TCCCCCAGGCTGTTCTCCAGGCTTACAGTCTGGTGCTTGGGAGAGTCAGGCAGGGTTAAAC  
TGCAGGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCCTCTACCAGTTGGCAG  
ACAGCCGTTTGTCTACATGGCTTTGATAATTGTTTGAGGGGAGGAGATGGAAACAATGTGG  
AGTCTCCCTCTGATTGGTTTTTGGGGAAATGTGGAGAAGAGTGCCCTGCTTTGCAAACATCAA  
CCTGGCAAAAATGCAACAAATGAATTTTCCACGCAGTTCTTTCCATGGGCATAGGTAAGCTG  
TGCCTTCAGCTGTTGCAGATGAAATGTTCTGTTACCCCTGCATTACATGTGTTTATTCATCC  
AGCAGTGTTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTC  
CCTCTCTCAGCACAGCCTGGGGAGGGGGTCAATTGTTCTCCTCGTCCATCAGGGATCTCAGAG  
GCTCAGAGACTGCAAGCTGCTTGCCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCAT  
CTGGTTGTGACTCTAAGCTCAGTGCTCTCTCCACTACCCACACCCAGCCTTGGTGCCACCAA  
AAGTGCTCCCCAAAAGGAAGGAGAATGGGATTTTTCTTGAGGCATGCACATCTGGAATTAAG  
GTCAAACATAATTCTCACATCCCTCTAAAAGTAACTACTGTTAGGAACAGCAGTGTTCTCAC  
AGTGTGGGGCAGCCGTCTTCTAATGAAGACAATGATATTGACACTGTCCCTCTTTGGCAGT  
TGCATTAGTAACCTTTGAAAGGTATATGACTGAGCGTAGCATAACAGGTTAACCTGCAGAAACA  
GTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTTGCAAAATCACTTAGCAGCAAC  
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGTGAAACATGGTT  
GTAATATGCGACTGCGAACAAGTGAAGTCTACGCCACTCCACAAATGATGTTTTTCAAGGTGTCA  
TGGACTGTTGCCACCATGTATTCATCCAGAGTTCTTAAAGTTTAAAGTTGCACATGATTGTA  
TAAGCATGCTTTCTTTGAGTTTTTAAATTATGTATAAACATAAGTTGCATTTAGAAATCAAGC  
ATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 84**

MQRLGATLLCLLLAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ  
HKLRSAVEEMEAEAAAKASSEVNLANLPPSYHNETNTDTKVGNNTIHVHREIHKITNNQTG  
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRDSECCG  
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGLCCAFQRGLLFPVCTPLPVEGELCHDPASRL  
LDLITWELEPDGALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV  
GSFMEEVRQELEDLERSLTEEMALGEPAAAAAALLGGEI

### **Signal sequence:**

amino acids 1-19

### **N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

### **Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

### **N-myristoylation site.**

amino acids 202-208, 217-223

### **Amidation site.**

amino acids 140-144



## FIGURE 85

AAGGAGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTCTGGGCTCAGAAGGACTCTG  
AAGATAACAATAATTTTCAGCCCATCCACTCTCCTTCCCTCCCAAACACACATGTGCATGTACACACACACATACA  
CACACATACACCTTCTCTCTTCACTGAAGACTCACAGTCACTCACTCTGTGAGCAGGTCATAGAAAAGGACAC  
TAAAGCCTTAAGGACAGGCCTGGCCATTACCTCTGCAGCTCCTTTGGCTTGTGAGTCAAAAAACATGGGAGGGG  
CCAGGCACGGTGACTCACACCTGTAATCCCAGCATTTTGGGAGACCGAGGTGAGCAGATCACTTGAGGTGAGGAG  
TTCGAGACCAGCCTGGCCAACATGGAGAAACCCCATCTCTACTAAAAATACAAAAATTAGCCAGGAGTGGTGGC  
AGGTGCCTGTAATCCCAGCTACTCAGGTGGCTGAGCCAGGAGAATCGCTTGAATCCAGGAGGCGGAGGATGCAGT  
CAGCTGAGTGCACCGCTGCACCTCCAGCCTGGGTGACAGAATGAGACTCTGTCTCAAACAAACAAACACGGGAGGA  
GGGGTAGATACTGCTTCTCTGCAACCTCCTTAACCTCTGCATCCTCTTCTTCCAGGGCTGCCCCGTATGGGGCCTG  
GCAATGACTGAGCAGGCCCAGCCCCAGAGGACAAGGAAGAGAAGGCATATTGAGGAGGGCAAGAAGTGACGCCCCG  
GTGTAGAATGACTGCCCTGGGAGGGTGGTTTCTTGGGCCCTGGCAGGGTGTCTGACCCCTTACCCCTGCAAAACACA  
AAGAGCAGGACTCCAGACTCTCCTTGTGAATGGTCCCCCTGCCCTGCAGCTCCACCATTGAGGCTTCTCGTGGCCCC  
ACTCTTGCTAGCTTGGGTGGCTGGTGCCACTGCCACTGTGCCCGTGGTACCCCTGGCATGTTCCCTGCCCCCCCTCA  
GTGTGCCTGCCAGATCCGGCCCTGGTATACGCCCCGCTCGTCTTACCAGGAGGCTACCCTGTGGAAATGCAATGA  
CCTATTCTGACGGCAGTCCCCCGGCCTCCCCGAGGCACACAGACCCTGCTCCTGCAGAGCAACAGCATTTGT  
CCGTGTGGACCAGAGTGAGCTGGGCTACCTGGCCAATCTCACAGAGCTGGACCTGTCCCAGAACAGCTTTTCGGA  
TGCCCCGAGACTGTGATTTCCATGCCCTGCCCCAGCTGCTGAGCCTGCACCTAGAGGAGAACCAGCTGACCCGGCT  
GGAGGACCACAGCTTTGACGGGCTGGCCAGCCTACAGGAACCTTATCTCAACCACAACCAGCTCTACCAGCATCGC  
CCCCAGGGCCTTTTCTGGCCTCAGCAACTTGCTGCGGCTGCACCTCAACTCCAACCTCCTGAGGGCCATTGACAG  
CCGCTGGTTTGAATGCTGCCCAACTTGGAGATACTCATGATTGGCGGCAACAAGGTAGATGCCATGCAATGA  
GAACCTTCCGGCCCCCTGGCCAACCTGCGTAGCCTGGTGCTAGCAGGCATGAACCTGCGGGAGATCTCCGACTATGC  
CCTGGAGGGGCTGCAAGCCTGGAGAGCCTCTCCTTCTATGACAACCAGCTGGCCCCGGGTGCCCAGGCGGGCCT  
GGAACAGGTGCCCGGGCTCAAGTTCTTAGACCTCAACAAGAACCCGCTCCAGCGGGTAGGGCCGGGGGACTTTGC  
CAACATGCTGCACCTTAAGGAGCTGGGACTGAACAACATGGAGGAGCTGGTCTCCATCGACAAGTTTGCCCTGGT  
GAACCTCCCCGAGCTGACCAAGCTGGACATACCAATAACCCACGGCTGTCTTTCATCCACCCCCGCGCCTTCCA  
CCACCTGCCCCAGATGGAGACCCTCATGCTCAACAACAACGCTCTCAGTGCCCTTGACACAGCAGACGGTGGAGTC  
CCTGCCCCAACCTGCAGGAGGTAGGTCTCCACGGCAACCCCATCCGCTGTGACTGTGTCTATCCGCTGGGCCAATGC  
CACGGGCACCCGTGTCCGCTTTCATCGAGCCGCAATCCACCCTGTGTGCGGAGCCTCCGGACCTCCAGCGCCTCCC  
GGTCCGTGAGGTGCCCTTCCGGGAGATGACGGACCACTGTTTGGCCCTCATCTCCCCACGAAGCTTCCCCCAAG  
CCTCCAGGTAGCCAGTGGAGAGAGCATGGTGCTGCATTGCCGGGCACTGGCCGAACCCGAACCCGAGATCTACTG  
GGTCACTCCAGCTGGGCTTCGACTGACACCTGCCCATGCAGGCAGGAGGTACCGGGTGTACCCCGAGGGGACCCCT  
GGAGCTGCGGAGGGTGACAGCAGAAGAGGCAGGGCTATACACCTGTGTGGCCAGAACCCTGGTGGGGGCTGACAC  
TAAGACGGTTAGTGTGGTTGTGGGCCGTGCTCTCCTCCAGCCAGGCAGGGACGAAGGACAGGGGCTGGAGCTCCG  
GGTGCAGGAGACCCACCCCTATCACATCCTGCTATCTTGGGTACCCCAACCAACAGTGTCCACCAACCTCAC  
CTGGTCCAGTGCCCTCCTCCCTCCGGGGCCAGGGGGCCACAGCTCTGGCCCGCCTGCCCTCGGGGAACCCACAGCTA  
CAACATTACCCGCTCCTTTCAGGCCACGGAGTACTGGGCCTGCCCTGCAAGTGGCCTTTGCTGATGCCCACACCCA  
GTTGGCTTGTGTATGGGCCAGGACCAAGAGGCCACTTCTTGCCACAGAGCCTTAGGGGATCGTCTGGGCTCAT  
TGCCATCCTGGCTCTCGCTGTCTTCTCCTGGCAGCTGGGCTAGCGGCCACCTTGGCACAGGCCAACCCAGGAA  
GGGTGTGGGTGGGAGGCGGCTCTCCCTCCAGCCTGGGCTTTCTGGGGCTGGAGTGCCCCCTTCTGTCCGGGTTGT  
GTCTGCTCCCTCGTCTGCCCTGGAATCCAGGGAGGAAGCTGCCAGATCCTCAGAAGGGGAGACACTGTTGCC  
ACCATTGTCTCAAAATTTCTTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGACTACTTTTTTACCAA  
AGAGAAGCAGTCTGGGCCAGATGCCCTGCCAGGAAAGGGACATGGACCCACGTGCTTGAGGCCTGGCAGCTGGGC  
CAAGACAGATGGGGCTTTGTGGCCCTGGGGGTGCTTCTGCAGCCTTGAAAAAGTTGCCCTTACCTCCTAGGGTCA  
CCTCTGCTGCCATTCTGAGGAACATCTCCAAGAACAGGAGGGACTTTGGCTAGAGCCTCCTGCCTCCCCATCTT  
CTCTCTGCCCAGAGGCTCCTGGGCTGGCTTGGCTGTCCCCTACCTGTGTCCCCGGGCTGCACCCCTTCTCTTTC  
TCTTTCTCTGTACAGTCTCAGTTGCTTGTCTTGTGCTCCTGGGCAAGGGCTGAAGGAGGCCACTCCATCTCAC  
CTCGGGGGGCTGCCCTCAATGTGGGAGTGACCCAGCCAGATCTGAAGGACATTTGGGAGAGGGATGCCAGGAA  
CGCCTCATCTCAGCAGCCTGGGCTCGGCATTCCGAAGCTGACTTTCTATAGGCAATTTTGTACCTTTGTGGAGAA  
ATGTGTACCTCCCCCAACCCGATTCACTCTTTCTCCTGTTTTGTAAAAAATAAAAAATAAATAACAATAAA  
AAAA

## **FIGURE 86**

MRLLVAPLLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA  
VPPALPAGTQTL LLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHL  
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE  
MLPNLEILMIGGNKVDAILDMNFRPLANLRSLVLAGMNLREISDYALEGLQSLESLSFYDNQ  
LARVPRRALEQVPGLKFLDLNKNPLQRVGP GDFANMLHLKELGLNNMEELV SIDKFALVNL P  
ELTKLDITNNPRLSFIHPRAFHHLPQMETLMLNNNALSALHQQTVESLPNLQEVGLHGNPIR  
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPSLQ  
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEGTLELRRVTAE EAGLYT  
CVAQNLVGADTKTVSVVVGRALLQPRDEGQGLELRVQETHPYHILLSWVTPPNTVSTNLTW  
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS  
CHRALGDRPGLIAIALAVLLLAAGLAHLGTGQPRKGVGGRRPLPPAWAFWGSAPSVRVV  
SAPLVLPWNPGRKLP RSSEGETLLPPLSQNS

### **Signal sequence:**

amino acids 1-18

### **Transmembrane domain:**

amino acids 629-648

### **N-glycosylation site.**

amino acids 94-98, 381-385, 555-559, 583-587

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 485-489

### **Casein kinase II phosphorylation site.**

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,  
243-247, 313-317, 488-492, 700-704

### **Tyrosine kinase phosphorylation site.**

amino acids 532-540

### **N-myristoylation site.**

amino acids 15-21, 493-499, 566-572

### **Amidation site.**

amino acids 470-474, 660-664, 692-696

# FIGURE 87

GCAAGCCAAGGCGCTGTTTTGAGAAGGTGAAGAAGTTCCGGACCCATGTGGAGGAGGGGGACATTGTGTACCGCCT  
 CTACATGCGGCAGACCATCATCAAGGTGATCAAGTTTCATCCTCATCATCTGCTACACCGTCTACTACGTGCACAA  
 CATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCACCC  
 CCTGGCCACACTCTTCAAGATCCTGGCGTCTTCTACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCATGTA  
 CACACTGTGGTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTTGAGTCGATCCGTGAGGAGAGCAGCTACAG  
 CGACATCCCCGACGTCAAGAACGACTTCGCCTTCATGCTGCACCTCATTGACCAATACGACCCGCTCTACTCCAA  
 GCGCTTCGCCGTCTTCTGTGCGGAGGTGAGTGAGAACAAGCTGCGGCAGCTGAACCTCAACAACGAGTGGACGCT  
 GGACAAGCTCCGGCAGCGGCTCACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTTTCATGCTCAGTGGCAT  
 CCTGACACTGTGTTTTGACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCCCGC  
 CAGCATTGCCCGAGCTCACGGGCCTCAAGGAGCTGTGGCTCTACCACACAGCGGCCAAGATTGAAGCGCCTGCGCT  
 GGCTTCTGCGCGAGAACCTGCGGGCGCTGCACATCAAGTTTACCAGACATCAAGGAGATCCCGCTGTGGATCTA  
 TAGCTGAAGACACTGGAGGAGCTGCACCTGACGGGCAACCTGAGCGCGGAGAACAACCGCTACATCGTCATCGA  
 CGGGCTGCGGGAGCTCAAACGCTCAAGGTGCTGCGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGGTGGTCA  
 AGATGTGGGCGTGACCTGCAGAAGCTGTCCATCAACAATGAGGGCACCAAGCTCATCGTCTCAACAGCCTCAA  
 GAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCACTCCATCTTCAGCCT  
 CCACAACCTGCAGGAGATTGACCTCAAGGACAACAACCTCAAGACCATCGAGGAGATCATCAGCTTCCAGCACCT  
 GCACCGCCTCACCTGCCTTAAGCTGTGGTACAACCACATCGCCTACATCCCCATCCAGATCGGCAACCTCACCAA  
 CCTGGAGCGCCTCTACCTGAACCGCAACAAGATCGAGAAGATCCCCACCCAGCTCTTCTACTGCCGCAAGCTGCG  
 CTACCTGGACCTCAGCCACAACAACCTGACCTTCTCCTGCGGACATCGGCCTCCTGCAGAACCTCCAGAACCT  
 AGCCATCACGGCCAACCGGATCGAGACGCTCCCTCCGGAGCTCTTCCAGTGCCGGAAGCTGCGGGCCCTGCACCT  
 GGGCAACAACGTGCTGCAGTCACTGCCCTCCAGGTGGGCGAGCTGACCAACCTGACGCAGATCGAGCTGCGGGG  
 CAACCGGCTGGAGTGCTGCGCTGTGGAGCTGGGCGAGTGCCCACTGCTCAAGCGCAGCGGCTTGGTGGTGGAGGA  
 GGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCCTGAGCGAG  
 GCCGGCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCGAGGGGAGGGCCTAGCTTCTCCCAG  
 AACTCCCGGACAGCCAGGACAGCCTCGCGGCTGGGCGAGGCTGGGGCCGCTTGTGAGTCAGGCCAGAGCGAGA  
 GGACAGTATCTGTGGGGCTGGCCCCCTTTTCTCCTCTGAGACTCACGTCCCCCAGGGCAAGTGCTTGTGGAGGAG  
 AGCAAGTCTCAAGAGCGCAGTATTTGGATAATCAGGGTCTCCTCCCTGGAGGCCAGCTCTGCCCCAGGGGCTGAG  
 TGCCACCAAGGTCCTGGGACCTCCTTTAGTTCTTGGTATTTATTTTTTCTCCATCTCCACCTCCTTCATCC  
 AGATAACTTATACATTTCCAAGAAAGTTGAGCCAGATGGAAGGTGTTGAGGAAAGGTGGGCTGCCTTTTCCCC  
 TTGTCTTATTTAGCGATGCCGCGGGCATTTAACACCCACCTGGACTTCAGCAGAGTGGTCCGGGGCGAACCCAG  
 CCATGGGACGGTCACCCAGCAGTGCCGGGCTGGGCTCTGCGGTGCGGTCCACGGGAGAGCAGGCCTCCAGCTGGA  
 AAGGCCAGGCCTGGAGCTTGCCCTCTTCACTTTTTGTGGCAGTTTTAGTTTTTTTGTTTTTTTTTTTTAAATCAA  
 AAACAATTTTTTTTAAAAAAAGCTTTGAAAATGGATGGTTTGGGTATTAAGAAAGAAAAAAACCTAAAAAA  
 AAAAGACACTAACGGCCAGTGAGTTGGAGTCTCAGGGCAGGTGGCAGTTTTCCCTTGAGCAAAGCAGCCAGACGT  
 TGAAGTGTGTTTCTTTTCCCTGGGCGCAGGGTGCAGGGTGTCTTCCGATCTGGTGTGACCTTGGTCCAGGAGTT  
 CTATTTGTTTCTGGGGAGGGAGGTTTTTTTGTGTTTTTTTGGGTTTTTTTTTGGTGTCTTGTCTTTCTCTCTCC  
 ATGTGTCTTGGCAGGCACTCATTTCTGTGGCTGTGCGCCAGAGGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAG  
 ACTCGGGTTGGCTAATCCCCGGATGAACGGTGTCTCATTCGCACCTCCCCCTCCTCGTGCTGCCCTGCCCTCTCCA  
 CGCACAGTGTAAAGGAGCCAAGAGGAGCCACTTCGCCCAGACTTTGTTTTCCCACCTCCTGCGGCATGGGTGTGT  
 CCAGTGCCACCGCTGGCCTCCGCTGCTTCCATCAGCCCTGTGCGCCACCTGGTCCCTTCATGAAGAGCAGACACTTA  
 GAGGCTGGTCCGGAATGGGGAGGTGCCCCCTGGGAGGGCAGGCGTTGGTTCCAAGCCGGTCCCGTCCCTGGCGC  
 CTGGAGTGCACACAGCCAGTCCGCACCTGGTGGCTGGAAGCCAACCTGCTTTAGATCACTCGGTCCCCACCTT  
 AGAAGGGTCCCCGCTTAGATCAATCAGTGGACACTAAGGCACGTTTTAGAGTCTCTTGTCTTAATGATTATGT  
 CCATCCGTCTGTCCGTCCATTTGTGTTTTCTGCGTCTGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG  
 CCTCTGACAACCATGAAGCAAAAATCCGTTACATGTGGGTCTGAACCTGTAGACTCGGTACAGTATCAAATAAA  
 ATCTATAACAGAAAAA

FIGURE 87

[illegible]

**Transmembrane domain:**

N-glycosylation site.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Casein kinase II phosphorylation site.

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

## FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGT  
CCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACT  
GGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG  
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCCTGGTCAT  
GTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACTTTGAGGAAATTGGGC  
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTT  
GTGGATAATCCCGTGGGCACTGGGTTCACTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA  
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG  
AATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCTTATGGAGGAAAAATGGCAGCTGGC  
ATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATCAAGTGCAACTTTGCGGGGGT  
TGCCTTGGGTGATTCTCTGGATCTCCCCGTGTTGATTTCGGTGCTCTCCTGGGGACCTTACCTGT  
ACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA  
CTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAAT  
GATCATTGAACAGAACACAGATGGGGTGAAGTTCTATAACATCTTAACTAAAAGCACTCCCA  
CGTCTACAATGGAGTCGAGTCTAGAATTACACAGAGCCACCTAGTTTGTCTTTGTGTCAGCGC  
CACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAA  
GCTCAAAATTATTCTCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTTTGTGAACA  
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC  
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTGAGGAGGCCTG  
GGTGCGGAAACTGAAGTGGCCAGAACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGT  
ACAGTGACCCTAAATCTTTGGAAACATCTGCTTTTGTCAAGTCTTACAAGAACCTTGCTTTC  
TACTGGATTCTGAAAGCTGGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGAT  
GATGAGACTGGTGACTCAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCT  
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCT  
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCT  
GGAGGCAATTTGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGAT  
TTGTTTTGATCAAAATAAAGGATGATAATAGATATTAA

## **FIGURE 90**

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC  
KNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGTGFSY  
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR  
GTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNKGLYRE  
ATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS  
QLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL  
IVDTMGQEAWRKLKWPPELPKFSQLKWKALYSDPKSLETSFAFVKSYKNLAFYWILKAGHMVP  
SDQGDMALKMMRLVTQQE

### **Signal sequence:**

amino acids 1-25

### **N-glycosylation site.**

amino acids 64-68, 126-130, 362-366

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 101-105

### **Casein kinase II phosphorylation site.**

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

### **N-myristoylation site.**

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,  
187-193, 195-201, 331-337, 332-338, 360-366

Table 1. Demographic characteristics of the study population	
Age (years)	Mean (SD)
Male	50.5 (10.5)
Female	51.5 (10.5)
Marital status	
Married	75.5%
Single	24.5%
Divorced	0.5%
Widowed	0.5%
Education (years)	Mean (SD)
Male	12.5 (2.5)
Female	12.5 (2.5)
Occupation	
Professional	15.5%
Managerial	10.5%
Technical	10.5%
Skilled	10.5%
Unskilled	10.5%
Homemaker	10.5%
Retired	10.5%
Unemployed	10.5%
Income (US\$)	Mean (SD)
Male	10,000 (5,000)
Female	10,000 (5,000)
Health insurance	
Yes	75.5%
No	24.5%
Smoking status	
Smoker	15.5%
Non-smoker	84.5%
Alcohol consumption	
Yes	15.5%
No	84.5%
Family size	Mean (SD)
Male	3.5 (1.5)
Female	3.5 (1.5)
Number of children	Mean (SD)
Male	2.5 (1.5)
Female	2.5 (1.5)
Number of grandchildren	Mean (SD)
Male	1.5 (1.5)
Female	1.5 (1.5)
Number of great-grandchildren	Mean (SD)
Male	0.5 (0.5)
Female	0.5 (0.5)
Number of great-great-grandchildren	Mean (SD)
Male	0.1 (0.1)
Female	0.1 (0.1)
Number of great-great-great-grandchildren	Mean (SD)
Male	0.05 (0.05)
Female	0.05 (0.05)
Number of great-great-great-great-grandchildren	Mean (SD)
Male	0.01 (0.01)
Female	0.01 (0.01)
Number of great-great-great-great-great-grandchildren	Mean (SD)
Male	0.005 (0.005)
Female	0.005 (0.005)
Number of great-great-great-great-great-great-grandchildren	Mean (SD)
Male	0.001 (0.001)
Female	0.001 (0.001)
Number of great-great-great-great-great-great-great-grandchildren	Mean (SD)
Male	0.0005 (0.0005)
Female	0.0005 (0.0005)
Number of great-great-great-great-great-great-great-great-grandchildren	Mean (SD)
Male	0.0001 (0.0001)
Female	0.0001 (0.0001)
Number of great-great-great-great-great-great-great-great-great-grandchildren	Mean (SD)
Male	0.00005 (0.00005)
Female	0.00005 (0.00005)
Number of great-great-great-great-great-great-great-great-great-great-grandchildren	Mean (SD)
Male	0.00001 (0.00001)
Female	0.00001 (0.00001)
Number of great-great-great-great-great-great-great-great-great-great-great-grandchildren	Mean (SD)
Male	0.000005 (0.000005)
Female	0.000005 (0.000005)
Number of great-great-great-great-great-great-great-great-great-great-great-great-grandchildren	Mean (SD)
Male	0.000001 (0.000001)
Female	0.000001 (0.000001)
Number of great-great-great-great-great-great-great-great-great-great-great-great-great-grandchildren	Mean (SD)
Male	0.0000005 (0.0000005)
Female	0.0000005 (0.0000005)
Number of great-great-great-great-great-great-great-great-great-great-great-great-great-great-grandchildren	Mean (SD)
Male	0.0000001 (0.0000001)
Female	0.0000001 (0.0000001)
Number of great-great-great-great-great-great-great-great-great-great-great-great-great-great-great-grandchildren	Mean (SD)
Male	0.00000005 (0.00000005)
Female	0.00000005 (0.00000005)
Number of great-great-great-great-great-great-great-great-great-great-great-great-great-great-great-great-grandchildren	Mean (SD)
Male	0.00000001 (0.00000001)
Female	0.00000001 (0.00000001)
Number of great-great-great-great-great-great-great-great-great-great-great-great-great-great-great-great-great-grandchildren	Mean (SD)
Male	0.000000005 (0.000000005)
Female	0.000000005 (0.000000005)
Number of great-great-great-great-great-great-great-great-great-great-great-great-great-great-great-great-great-great-grandchildren	Mean (SD)
Male	0.000000001 (0.000000001)
Female	0.000000001 (0.000000001)
Number of great-great-great-great-great-great-great-great-great-great-great-great-great-great-great-great-great-great-great-grandchildren	Mean (SD)
Male	0.0000000005 (0.0000000005)
Female	0.0000000005 (0.0000000005)
Number of great-grandchildren	Mean (SD)
Male	0.0000000001 (0.0000000001)
Female	0.0000000001 (0.0000000001)
Number of great-grandchildren	Mean (SD)
Male	0.00000000005 (0.00000000005)
Female	0.00000000005 (0.00000000005)
Number of great-grandchildren	Mean (SD)
Male	0.00000000001 (0.00000000001)
Female	0.00000000001 (0.00000000001)
Number of great-grandchildren	Mean (SD)
Male	0.000000000005 (0.000000000005)
Female	0.000000000005 (0.000000000005)
Number of great-grandchildren	Mean (SD)
Male	0.000000000001 (0.000000000001)
Female	0.000000000001 (0.000000000001)</

GGCCGCGGGAGAGGAGGCCATGGGCGCGCGCGGGGCGCTGCTGCTGGCGCTGCTGCTGGCTC  
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCGCCGTTATCAGGACCATGCGGCCGA  
CGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCGAACTCGGGCGTTGGCCGTGGCA  
GGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG  
CACTCACGGCGGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG  
GTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTACTACACCCG  
TTA<sup>1</sup>CTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTACCCCTATGACATTG  
CCTTGGTGAAGCTGTCTGCACCTGTCACCTACACTAAACACATCCAGCCCATCTGTCTCCAG  
GCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGGTACATCAA  
AGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCAGGTCGCCATCATAAACA  
ACTCTATGTGCAACCACCTCTTCCTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGACATG  
GTTTGTGCTGGCAACGCCCAAGGCGGGAAGGATGCCTGCTTCGGTGACTCAGGTGGACCCTT  
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTGGGCTGTG  
GTCGGCCCAATCGGCCCCGGTGTCTACACCAATATCAGCCACCAC<sup>2</sup>TTTGAGTG<sup>3</sup>GATCCAGAAG  
CTGATGGCCCAGAGTGGCATGTCCCAGCCAGACCCCTCCTGGCCACTACTCTTTTTTCCCTCT  
TCTCTGGGCTCTCCCACTCCTGGGGCCGGTCTTGAGGCCTACCTGAGCCCATGCAGCCTGGGGC  
CACTGCCAAGTCAGGCCCTGGTTCTCTTCTGTCTTGT<sup>4</sup>TTGGTAATAAACACATTCCAGTTGA  
TGCCTTGCAGGGCATTCCTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 92**

MGARGALLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSRLRW  
DSHVCVSVLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI  
YLSPRYLGNSPYDIALVKLSAPVTTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP  
SPHTLQEVQVAIINNSMCNHLFLKYSFRKDI FGDMVCAGNAQGGKDACFGDSGGPLACNKNG  
LWYQIGVVSWSGVGCGRPNRPGVYTNI SHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL  
LGPV

### **Signal sequence:**

amino acids 1-18

### **N-glycosylation site.**

amino acids 167-171, 200-204, 273-277

### **Casein kinase II phosphorylation site.**

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

### **N-myristoylation site.**

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,  
259-265, 269-275

### **Amidation site.**

amino acids 33-37

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 252-263,

### **Serine proteases, trypsin family, histidine active site.**

amino acids 78-84



## FIGURE 93

CCCCACGCGTCCGCGGACGCGTGGAAGGGCAGAATGGGACTCCAAGCCTGCCTCCTAGGGCT  
CTTTGCCCCATCCTCTCTGGCAAATGCAGTTACAGCCCGGAGCCCGACCAGCGGAGGACGC  
TGCCCCCAGGCTGGGTGTCCCTGGGCCGTGCGGACCCTGAGGAAGAGCTGAGTCTCACCTTT  
GCCCTGAGACAGCAGAATGTGGAAAGACTCTCGGAGCTGGTGCAGGCTGTGTGCGATCCCAG  
CTCTCCTCAATACGGAATAACCTGACCCTAGAGAATGTGGCTGATCTGGTGAGGCCATCCC  
CACTGACCCTCCACACGGTGCAAAAATGGCTCTTGGCAGCCGGAGCCCAGAAGTGCCATTCT  
GTGATCACACAGGACTTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC  
TGGGGCTGAGTTTCATCACTATGTGGGAGGACCTACGGAAACCCATGTTGTAAGGTCCCCAC  
ATCCCTACCAGCTTCCACAGGCCTTGGCCCCCATGTGGACTTTGTGGGGGGACTGCACCGT  
TTTCCCCCAACATCATCCCTGAGGCAACGTCTGAGCCGCAGGTGACAGGGACTGTAGGCCT  
GCATCTGGGGGTAAACCCCTCTGTGATCCGTAAGCGATACTGACCTCACAAGACGTGG  
GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCCTGGAGCAGTATTTCCATGAC  
TCAGACCTGGCTCAGTTCATGCGCCTCTTCGGTGGCAACTTTGCACATCAGGCATCAGTAGC  
CCGTGTGGTTGGACAACAGGGCCGGGGCCGGGCGGGGATTGAGGCCAGTCTAGATGTGCAGT  
ACCTGATGAGTGCTGGTGCCAAACATCTCCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG  
GGACAGGAGCCCTTCTGCAGTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT  
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCCTACATCCAGCGGGTCA  
ACACTGAGCTCATGAAGGCTGCCGCTCGGGGTCTCACCCTGCTCTTCGCCTCAGGTGACAGT  
GGGGCCGGGTGTTGGTCTGTCTCTGGAAGACACCAGTTCGCGCCTACCTTCCCTGCCTCCAG  
CCCCTATGTCAACCACAGTGGGAGGCACATCCTTCCAGGAACCTTTCCTCATCACAATGAAA  
TTGTTGACTATATCAGTGGTGGTGGCTTCAGCAATGTGTTCCCACGGCCTTCATACCAGGAG  
GAAGCTGTAACGAAGTTCCTGAGCTCTAGCCCCACCTGCCACCATCCAGTTACTTCAATGC  
CAGTGGCCGTGCCTACCCAGATGTGGCTGCACCTTCTGATGGCTACTGGGTGGTCAGCAACA  
GAGTGCCCATTCATGGGTGTCCGGAACCTCGGCCTCTACTCCAGTGTTTGGGGGGATCCTA  
TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCCCTCTTGGCTTTCTCAACCCAAG  
GCTCTACCAGCAGCATGGGGCAGGTCTCTTTGATGTAACCCGTGGCTGCCATGAGTCCTGTC  
TGGATGAAGAGGTAGAGGGCCAGGGTTTCTGCTCTGGTCTGGCTGGGATCCTGTAACAGGC  
TGGGGAACACCAACTTCCCAGCTTTGCTGAAGACTCTACTCAACCCCTGACCCCTTCTCTATC  
AGGAGAGATGGCTTGTCCCCTGCCCTGAAGCTGGCAGTTCAGTCCCTTATTCTGCCCTGTTG  
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCTGAAA  
TGCTGTGAGCTTGACTTGACTCCCAACCCCTACCATGCTCCATCATACTCAGGTCTCCCTACT  
CCTGCCTTAGATTCTCTCAATAAGATGCTGTAACTAGCATTTTTTTGAATGCCTCTCCCTCCGC  
ATCTCATCTTTCTCTTTTCAATCAGGCTTTTCCAAAGGGTTGTATACAGACTCTGTGCACTA  
TTTCACTTGATATTCATTCCCCAATTCACTGCAAGGAGACCTCTACTGTCACCGTTTACTCT  
TTCCTACCCTGACATCCAGAAACAATGGCCTCCAGTGCATACTTCTCAATCTTTGCTTTATG  
GCCTTTCCATCATAGTTGCCCACTCCCTCTCCTTACTTAGCTTCCAGGTCTTAACCTCTCTG  
ACTACTCTTGTCTTCTCTCTCATCAATTTCTGCTTCTTCATGGAATGCTGACCTTCATTGC  
TCCATTTGTAGATTTTTGCTCTTCTCAGTTTACTCATTTGTCCCCTGGAACAAATCACTGACA  
TCTACAACCATTACCATCTCACTAAATAAGACTTCTATCCAATAATGATTGATACCTCAAA  
TGTAACAAAA

## **FIGURE 94**

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEELSLTFALRQQNVERLS  
ELVQAVSDPSSPQYGKYLTLNVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL  
SIRQAELLPLPGAEFHHYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGGLHRFPPTSSLRQRP  
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVGSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG  
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMASAGANISTWVYSSPGRHEGQEPFLQWLML  
LSNESALPHVHTVSYGDDDEDLS SAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVSGRH  
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGF SNVFP RPSYQEEAVTKFLSSSP  
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG  
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

### **Signal sequence:**

amino acids 1-16

### **N-glycosylation site.**

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

### **Glycosaminoglycan attachment site.**

amino acids 361-365, 408-412, 538-542

### **Casein kinase II phosphorylation site.**

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

### **N-myristoylation site.**

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,  
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,  
521-527, 533-539, 549-555

[illegible][illegible]

## **FIGURE 96**

MAGIPGLLFLLFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVS  
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIIYLSSSGDGAQHRDSGSSGKS  
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKG  
TQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKNANDIGMDYDYA  
LLELKPKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCD  
AQPASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYW  
IKGNYLDCREG

### **Signal sequence:**

amino acids 1-19

### **N-glycosylation site.**

amino acids 93-97, 207-211

### **Glycosaminoglycan attachment site.**

amino acids 109-113, 316-320

### **Casein kinase II phosphorylation site.**

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

### **N-myristoylation site.**

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

### **Serine proteases, trypsin family, histidine active site.**

amino acids 171-177

[illegible]

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCCATGGTGGTTT  
CTGGAGCGCCCCCAGCCCTGGGTGGGGGCTGTCTCGGCACCTTCACCTCCCTGCTGCTGCTG  
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCCAGCCTGTGGGAAGCCCCA  
GCAGCTGAACCGGGTGTGTTGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA  
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCTGGGTGATC  
ACTGCTGCCCCTGTTTCAAGGACAACCTGAACAAACCATAACCTGTTCTCTGTGCTGCTGGG  
GGCCTGGCAGCTGGGGAAACCCTGGCTCTCGGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC  
CCCACCCTGTGTATTCTTGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCGTCTCGAG  
CGCTCCATACAGTTCTCAGAGCGGGTCTTGCCCATCTGCCTACCTGATGCCTCTATCCACCT  
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGGAGCATCCAAGATGGAGTTCCTTG  
CCCACCCTCAGACCCTGCAGAAGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT  
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGTGCCGGCTACTT  
GGAGGGGGAGCGGGATGCTTGTCTGGGCGACTCCGGGGGCCCCCTCATGTGCCAGGTGGACG  
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCGAGCGCAACAGGCC  
GGGGTCTACATCAGCCTCTCTGCGCACCGCTCCTGGGTGGAGAAGATCGTGCAAGGGGTGCA  
GCTCCGCGGGGCGGCTCAGGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCG  
CCGCGCGCTCTAGGGCGCAGCGGGACGCGGGGCTCGGATCTGAAAGGCGGCCAGATCCACA  
TCTGGATCTGGATCTGCGGCGGCCTCGGGCGGTTTCCCCCGCCGTAAATAGGCTCATCTACC  
TCTACCTCTGGGGGCCCGGACGGCTGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCCGAC  
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCCGCCCAACGGCCTCATGTCCCCGCCCCCAC  
GACTTCCGGCCCCGCCCCGGGCCCCAGCGCTTTTGTGTATATAAATGTTAATGATTTTTAT  
AGGTATTTGTAACCCTGCCCACATATCTTATTTATTCTTCCAATTTCAATAAATTATTTAT  
CTCCAAAAAAAAAAAA

## **FIGURE 98**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318

><subunit 1 of 1, 317 aa, 1 stop

><MW: 33732, pI: 7.90, NX(S/T): 1

MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWP  
WIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVA  
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPNTHCWISGWGSIQDG  
VPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLGDSGGPLMC  
QVDGAWLLAGIISWGECAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQG  
SGAAARS

### **Signal sequence:**

amino acids 1-32

### **N-glycosylation site.**

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

### **Glycosaminoglycan attachment site.**

amino acids 826-830

### **Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

### **Tyrosine kinase phosphorylation site.**

amino acids 607-615

### **N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTTCCTGATGCTTCTGCTGCCGCTACTGCTA  
CTGCTGGTGGCCACCACAGGCCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGATGGT  
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA  
GATGGGACGAGGAGCTGGCCGCCTTCGCCAAGGCCTACGCACGGCAGTGCCTGTGGGGCCAC  
AACAAGGAGCGCGGGCGCCGCGGCGAGAATCTGTTTCGCCATCACAGACGAGGGCATGGACGT  
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT  
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATC  
GGCTGTGGTTCCCACTTCTGTGAGAAGCTCCAGGGTGTTGAGGAGACCAACATCGAATTACT  
GGTGTGCAACTATGAGCCTCCGGGGAACGTGAAGGGGAAACGGCCCTACCAGGAGGGGACTC  
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC  
CCGGAAGATGCTCAGGATTTGCCTTACCTGGTAAGTGAAGGGCCCATCCTTCCGGGCGACTGA  
AGCATCAGACTCTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCT  
TGGTAAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCC  
CCAACTTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCGTAAC  
AACTGAGGTCCCTTCCATTTTGGCAGCTCACAGCCTGCCCTCCTTGATGAGGAGCCAGTTA  
CCTTCCCCAAATCGACCCATGTTCCCTATCCCCAAATCAGCAGACAAAGTGACAGACAAAACA  
AAAGTGCCCTCTAGGAGCCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGGCAAG  
GGAATCCTACCCCATGCCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCTTCCAGTG  
AGGTCTTGGCCTCAGTTTTTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC  
CACACGGGGCACACCTCCTCCAAGTCCCTGCCCAATTTCCCCAATACCTCTGCCACCGCTAA  
TGCCACGGGTGGGCGTGCCCTGGCTCTGCAGTCGTCTTGCCAGGTGCAGAGGGGCCCTGACA  
AGCCTAGCGTTGTGTGAGGGCTGAACTCGGGCCCTGGTCATGTGTGGGGCCCTCTCCTGGGA  
CTACTGCTCCTGCCTCCTCTGGTGTGGCTGGAATCTTCTGAATGGGATACCACTCAAAGGG  
TGAAGAGGTCAGCTGTCTCCTGTCATCTTCCCCACCCTGTCCCCAGCCCCCTAAACAAGATA  
CTTCTTGGTAAAGGCCCTCCGGAAGGGAAAGGCTACGGGGCATGTGCCTCATCACACCATCC  
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCGCCTGAGGACTGCACACC  
GGGCCCACACCTCTCCTGCCCCCTCCCTCCTGAGTCCTGGGGGTGGGAGGATTTGAGGGAGCT  
CACTGCCTACCTGGCCTGGGGCTGTCTGCCCACACAGCATGTGCGCTCTCCTGAGTGCCTG  
TGTAGCTGGGGATGGGGATTCTAGGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGGTTCT  
TTTGAGTGGGGGAGGCAGGGACGAGGGAAGGAAAGTAACTCCTGACTCTCCAATAAAAACCT  
GTCCAACCTGTGAAA

Figure 1 consists of 12 histograms arranged in a single column. Each histogram represents the distribution of the number of non-zero elements in the vector  $x$  for a specific value of  $n$ . The values of  $n$  are 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, and 120. The x-axis for each histogram is labeled 'Number of non-zero elements' and ranges from 0 to  $n$ . The y-axis is labeled 'Frequency' and ranges from 0 to 10. The histograms show that as  $n$  increases, the distribution of non-zero elements shifts to the right, with the peak frequency increasing and the range of non-zero elements expanding.

Signal sequence:

N-glycosylation site.

Glycosaminoglycan attachment site.

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,  
250-256

Amidation site.

amino acids 82-86, 172-176

**Peroxidases proximal heme-ligand signature.**

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.**

amino acids 160-172



# FIGURE 101

GTAAGTGAAGTCAGGCTTTTCATTTGGGAAGCCCCCTCAACAGAATTCGGTCATTCTCCAAGTTATGGTGGACGT  
ACTTCTGTTGTTCTCCCTCTGCTTGTCTTTTTCACATTAGCAGACCGGACTTAAAGTCACAACAGATTATCTTTTCAT  
CAAGGCAAGTTCATGAGCCACCTTCAAAGCCTTCGAGAAGTGAACCTGAACAACAATGAATTGGAGACCATTCC  
AAATCTGGGACCAGTCTCGGCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGA  
ACATCTGAAAGAGTTTCAGTCCCTTGAACCTTTGGACCTTAGCAGCAACAATATTTTCAGAGCTCCAAACTGCATT  
TCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTTGACAA  
TTTGGCCAAACACTCTCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTTAAACT  
GCCCCAAGTGAACATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTTCCAAGCCTTGG  
TGCTCTGAAGTCTCTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTTGGGGGCTGAGCAA  
CATGGAAATTTTGAGCTGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTTACGGCTTGCTGATGCT  
GCAGGAACCTTCATCTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCCCTGGGAGTTCTGCCAGAAGCTCAG  
TGAGCTGGACCTAACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAATAC  
ACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCCTTCGGGGGCTTTCCAGTTTAAAGACTTT  
GGATCTGAAGAACAATGAAATTTCTGGACTATTGAAGACATGAATGGTGCCTTTCTCTGGGCTTGACAAACTGAG  
GCGACTGATACTCCAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCA  
TCTAGACCTGAGTGACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCAAAATGAAGAACTGCAACAAT  
GCATTTAAATACATCAAGCCTTTTGTGCGATTGGCAGCTAAAATGGCTCCACAGTGGGTGGCGAAAAACAAT  
TCAGAGCTTTGTAAATGCCAGTTGTGCCCATCTCAGCTGCTAAAAGGAAGAAGCATTTTGTCTGTTAGCCAGA  
TGGCTTTGTGTGTGATGATTTTCCCAAACCCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAGGTTTC  
CAATTTGAGTTTCATCTGCTCAGCTGCCAGCAGCAGTGAATCCCAATGACTTTTGTCTGGAAAAAGACAATGA  
ACTACTGCATGATGCTGAAATGGAATTTATGCACACCTCCGGGCCCAAGGTGGCGAGGTGATGGAGTATACCA  
CATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAATATCAGTGTGTCTCTCAATCACTTGGTTTC  
ATCCTACTCTGTCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTACCAAGACCCCCATGGATCTCACCAT  
CCGAGCTGGGGCCATGGCAGCTTGGAGTGTGCTGTGTTGGGGCAGCCAGCCCCCAGATAGCCTGGCAGAAAGGA  
TGGGGGCACAGACTTCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCGAGGATGACGTGTTCTTTATCGT  
GGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTTCAGCAATGC  
AACTCTGACTGTCTAGAAACACCATCATTTTTCGGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGC  
CGTCTACAGTGCATTGCTGGAGGAAGCCCTCCCCCTAAACTGAAGTGGACCAAGATGATAGCCCATTTGGTGGT  
ATTTTTCTTACCACAACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGC  
CACAGATCTGTTTCTTTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCAGA  
TCCTTTTGAACATATCATAAGGTTGCAGTCTTGACCAAGAAGCTTTTAAATGGACCACTATGAGCCCAAGTTA  
CATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCTTCAGAAGAATCCTGCGAACGGAGCTTCAGTAATATATC  
GTGGCCTTCACATGTGAGGAAGCTACTTAACACTAGTTACTCTCAATGAAGGACCTGGAATGAAAAATCTGTG  
TCTAAACAAGTCTCTTTAGATTTTAGTGCAATCCAGAGCCAGCGTCGGTTGCCCTCGAGTAATCTTTTCATGGG  
TACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAGCCATCAGATTGTCAGCC  
AAGAGCCTTTTATTTGAAAGCTCATTCTTCCCAGACTTGGACTCTGGGTGAGAGGAAGATGGGAAAGAAAGGAC  
AGATTTTCAGGAAGAAAATCACATTTGTACCTTTAAACAGACTTTAGAAAACACAGGACTCCAAATTTTCAGTC  
TTATGACTTGGACACATAGACTGAATGAGACCAAGGAAAAGCTTAACATACTACCTCAAGTGAACCTTTTATTTA  
AAAGAGAGAGAATCTTATGTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAAAATGCTTTATTTATACAGAT  
GAACCAAAATTACAAAAGTTATGAAAATTTTATACTGGGAATGATGCTCATATAAGAATACCTTTTTTAAACTA  
TTTTTTAACTTTGTTTTATGCAAAAAGTATCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTT  
TTATAATGCCAGATTTCTTTTTATGAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTACCATTTT  
TTAAATAGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAATGTGTCAATTTGAA

CCGTTCTGTTGTTCTCCCTCTGCTTGTCTTTTTCACATTAGCAGACCGGACTTAAAGTCACAACAGATTATCTTTTCAT

## **FIGURE 102**

MVDVLLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSAN  
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP  
GYFDNLANTLLVLKLNRRNRI SAIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKM  
QRNGVTKLMDGAFWGLSNMEILQLDHNNLTETTKGWLYGLLMLQELHLSQNAINRISPDAWE  
FCQKLSLDELTFNHL SRLDDSSFLGSLNLT LHIGNNRVSYIADCAFRGLSSSLKTLDLKNNE  
ISWTIEDMNGAFSGLDKLRRLLIQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQ  
MKKLQQLHLNLTSSLLCDCQLKWLPQWVAENNFSFVNASCAHPQLLKGRSIFAVSPDGFVCD  
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELLHDAEMENY AHLRAQG  
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGA  
MARLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN  
SAGSISANATLTVLETPSFLRPLLDRTVTKTGETAVLQCIAGGSPPPKNLWTKDDSPLVVTER  
HFFAAGNQLLIIVDSVDSDAGKYTCEMSNTLGTGERGNVRLSVIPTPTCDSPQMTAPSLDDD  
G WATVGVVIIAVVCCVVGTSLVWVVI IYHTRRRNEDCSITNTDETNPADIPSYLSSQGT  
LAD RQDGYVSSSESGSHHQFVTSSGAGFFLPQHDSSTCHIDNSSEADVEAATDLFLCPFLG  
STGP MYLKGNVYGSDPFETYHTGCSPDPRTVLMDHYEPSYIKKKECYPCSHPSSEESCERS  
FSNISW PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLD FSANPEPASVASSNSFMGTFGKALRR  
PHLDA YSSFGQPSDCQPRAFYLKAHSSPDLD SGSEEDGKERTDFQEENHICTFKQTL  
ENYRTPNFQS YDLDT

### **Signal sequence:**

amino acids 1-19

### **Transmembrane domain:**

amino acids 746-765

### **N-glycosylation site.**

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

### **Glycosaminoglycan attachment site.**

amino acids 826-830

### **Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

### **Tyrosine kinase phosphorylation site.**

amino acids 607-615

### **N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAAATG  
AAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGAAC  
GAAGCTTTTTCTTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA  
TAAACCAGAGTTAGACCCGCGGGGGTTGGTGTGTTCTGACATAAAATAAATAATCTTAAAGCAGCTGTTCCCTCC  
CCACCCCCAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTACAAAAGAAAAAGTATGTTTATTTTTCTC  
TATAAAGGAGAAAGTGAGCCAAGGAGATATTTTTGGAATGAAAAGTTTGGGGCTTTTTTAGTAAAGTAAAGAACT  
GGTGTGGTGGTGTTCCTTTCTTTTTGAATTTCCACAAAGAGGAGAGGAAATTAATAATACATCTGCAAAAGAAA  
TTTCAGAGAAGAAAAGTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAAACAGCAGAGCACAGTTGGA  
TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTTTCTTCATCAACCTCCTTTTTTTTAAAT  
TTTTATTCCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTCTTAACCACCTGGATTTCCATCTGGATGTTGCT  
GTGATCAGTCTGAAATACAACCTGTTTGAATTCAGAAGGACCAACACCAGATAAATTATGAATGTTGAACAAGAT  
GACCTTACATCCACAGCAGATAATGATAGGTCTTAGGTTTAACAGGGCCCTATTTGACCCCTGCTTGTGGTGTCT  
GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGCGGGCTCAGACCTGCCCTTCTGTGTGCTCCTGCAGCAA  
CCAGTTTCAAGGTGATTTGTGTTCCGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCCACCAACACACGGCT  
GCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAGGCACTTGGAATCCT  
ACAGTTGAGTAGGAACCATATCAGAACCATTGAAATTGGGGCTTCAATGGTCTGGCGAACCTCAACACTCTGGA  
ACTCTTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTTGTATACTTGTCTAAACTGAAGGAGCTCTGGTT  
GCGAAACAACCCCATGAAAGCATCCCTTCTTATGCTTTTAACAGAATTCCTTCTTTCGCGCCGACTAGACTTAGG  
GGAATTGAAAAGACTTTTCATACATCTCAGAAGGTGCCCTTGAAGGTCTGTCCAACCTTGAGGTATTTGAACCTTGC  
CATGTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAAACTAGATGAGCTGGATCTTTCTGGGAATCA  
TTTATCTGCCATCAGGCTGGCTCTTTCCAGGGTTTGTATGCACCTTCAAAAACTGTGGATGATACAGTCCAGAT  
TCAAGTGATTGAACGGAATGCCCTTTGACAACCTTCAGTCACTAGTGGAGATCAACCTGGCACACAATAATCTAAC  
ATTACTGCCTCATGACCTCTTCACTCCCTTGCATCATCTAGAGCGGATACATTTACATCACAAACCTTGGAAGTG  
TAACTGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTGTGCCCCGGTG  
TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCACATGCTATGCTCCGGT  
GATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCTGAGCTGAAATGTGCGGCCTCCACATC  
CCTGACATCTGTATCTTGGATTACTCCAAATGGAACAGTCATGACACATGGGGCGTACAAAGTGCGGATAGCTGT  
GCTCAGTGATGGTACGTTAAATTTACAAATGTAACGTGTGCAAGATACAGGCATGTACACATGTATGGTGAGTAA  
TTCCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCAACCACTACTCCTTTCTCTTACTTTTC  
AACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGGACCACAGATAACAATGTGGGTCCCACTCC  
AGTGGTCGACTGGGAGACCACCAATGTGACCACCTCTCTCACACCAAGAGCACAAGGTGACAGAGAAAAACCTT  
CACCATCCCAGTGACTGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCATGAAGACTACCAAAATCATCAT  
TGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTCTACAAGATGAGGAAGCAGCACC  
TCGGCAAAACCATCACGCCCCAACAAAGGACTGTTGAAATTATTAATGTGGATGATGAGATTACGGGAGACACACC  
CATGGAAGCCACCTGCCCATGCCGTCTATCGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTT  
CAACCACACAACAACAGTTAACACAATAAATTCAATACACAGTTTCACTGATGAACCGTTATTGATCCGAATGAA  
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTTACAGAGTTACAAAAAACAAACAATCAAAAAA  
GACAGTTTATTAATAATGACACAAATGACTGGGCTAAATCTACTGTTTCAAAAAAGTGCTTTTACAAAAA  
AAAAGAAAAGAAATTTATTTATTAATAATCTATTTGTGATCTAAAGCAGACAAAA

## **FIGURE 104**

MLNKMTLHPQQIMIGPRFNRALFDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKVIC  
VRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA  
NLNTLELFDNRLTTIPNGAFVYLSKLELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS  
YISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLELDLSGNHLSAIRPGSFQGLMHLQKL  
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNCDIL  
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE  
LKCRASSTLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTQDTGMYTCMVSNVGN  
TTASATLNVTAATTTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ  
STRSTEKTFTIPVTDINSIGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHRQN  
HHAPTRTVEIINVDDEITGDTPMESHLPMPAIEHEHLNHYSYKSPFNHTTTVNTINSIHSS  
VHEPLLIRMNSKDNVQETQI

### **Signal sequence:**

amino acids 1-44

### **Transmembrane domain:**

amino acids 523-543

### **N-glycosylation site.**

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,  
442-446, 488-492, 606-610

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

### **Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

### **N-myristoylation site.**

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,  
391-397, 422-428, 433-439, 531-537

Variable	Mean	SD	Min	Max
Age	34.5	10.2	21	55
Gender	0.5	0.5	0	1
Marital status	0.6	0.5	0	1
Education	12.5	1.5	9	16
Income	1500	500	500	3000
Health status	0.8	0.2	0	1
Smoking status	0.3	0.5	0	1
Alcohol consumption	0.2	0.4	0	1
Exercise frequency	0.5	0.5	0	1
Stress level	0.7	0.3	0	1
Sleep quality	0.6	0.4	0	1
Work satisfaction	0.5	0.5	0	1
Life satisfaction	0.7	0.3	0	1
Depression score	0.4	0.5	0	1
Anxiety score	0.3	0.4	0	1
Quality of life	0.6	0.4	0	1
Healthcare utilization	0.5	0.5	0	1
Health insurance status	0.9	0.1	0	1
Chronic disease status	0.2	0.4	0	1
Family size	2.5	1.0	1	5
Religious beliefs	0.5	0.5	0	1
Community involvement	0.4	0.5	0	1
Work-life balance	0.6	0.4	0	1
Perceived stress	0.7	0.3	0	1
Resilience score	0.5	0.5	0	1
Optimism score	0.6	0.4	0	1
Gratitude score	0.5	0.5	0	1
Self-efficacy score	0.6	0.4	0	1
Life purpose score	0.5	0.5	0	1
Meaning in life score	0.6	0.4	0	1
Positive psychology score	0.5	0.5	0	1
Well-being score	0.6	0.4	0	1
Life satisfaction score	0.7	0.3	0	1
Quality of life score	0.6	0.4	0	1
Health status score	0.8	0.2	0	1
Smoking status score	0.3	0.5	0	1
Alcohol consumption score	0.2	0.4	0	1
Exercise frequency score	0.5	0.5	0	1
Stress level score	0.7	0.3	0	1
Sleep quality score	0.6	0.4	0	1
Work satisfaction score	0.5	0.5	0	1
Life satisfaction score	0.7	0.3	0	1
Depression score	0.4	0.5	0	1
Anxiety score	0.3	0.4	0	1
Quality of life score	0.6	0.4	0	1
Healthcare utilization score	0.5	0.5	0	1
Health insurance status score	0.9	0.1	0	1
Chronic disease status score	0.2	0.4	0	1
Family size score	2.5	1.0	1	5
Religious beliefs score	0.5	0.5	0	1
Community involvement score	0.4	0.5	0	1
Work-life balance score	0.6	0.4	0	1
Perceived stress score	0.7	0.3	0	1
Resilience score	0.5	0.5	0	1
Optimism score	0.6	0.4	0	1
Gratitude score	0.5	0.5	0	1
Self-efficacy score	0.6	0.4	0	1
Life purpose score	0.5	0.5	0	1
Meaning in life score	0.6	0.4	0	1
Positive psychology score	0.5	0.5	0	1
Well-being score	0.6	0.4	0	1
Life satisfaction score	0.7	0.3	0	1
Quality of life score	0.6	0.4	0	1
Health status score	0.8	0.2	0	1
Smoking status score	0.3	0.5	0	1
Alcohol consumption score	0.2	0.4	0	1
Exercise frequency score	0.5	0.5	0	1
Stress level score	0.7	0.3	0	1
Sleep quality score	0.6	0.4	0	1
Work satisfaction score	0.5	0.5	0	1
Life satisfaction score	0.7	0.3	0	1
Depression score	0.4	0.5	0	1
Anxiety score	0.3	0.4	0	1
Quality of life score	0.6	0.4	0	1
Healthcare utilization score	0.5	0.5	0	1
Health insurance status score	0.9	0.1	0	1
Chronic disease status score	0.2	0.4	0	1
Family size score	2.5	1.0	1	5
Religious beliefs score	0.5	0.5	0	1
Community involvement score	0.4	0.5	0	1
Work-life balance score	0.6	0.4	0	1
Perceived stress score	0.7	0.3	0	1
Resilience score	0.5	0.5	0	1
Optimism score	0.6			

ACTTCATTATATTTGCACATTATATTTAATAAAATGTGTCAATTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCPTTCRCLGDLDDCSR  
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSPANIT  
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY  
FDNLANTLLVLKLNRRNRI SAIPPKMFKLPLQLQHLELNRNKIKNVDGLTFQGLGALKSLKMQR  
NGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWEFC  
QKLSELDLTFNHL SRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSSLKTLDLKNNEIS  
WTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK  
KLQQLHLNTSSLLCDCQLKWLPQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCDDF  
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELHDAEMENY AHLRAQGGE  
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGAMA  
RLECAAVGHPAPQIAWQKDGGTD FPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA  
GSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKNLWTKDDSPLVVTERHF  
FAAGNQLLIIVDSVDSDAGKYTCEMSNTLGTGERGNVRLSVIPTPTCDSPQMTAPSLDDD GWA  
TVGVVIIAVVCCVVGTSLVVVIIYHTRRNEDCSITNTDETNPADIPSYLSSQGT LADRQ  
DGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY  
LKGNVYGSDFPETYHTGCSPDPRTVLM DHYEPSYIKKKECYPCHPSEESCERSFSNISWPS  
HVRKLLNTSYSHNEGPGMKNLCLNKSSLD FSANPEPASVASSNSFMGTFGKALRRPHLDAYS  
SFGQPSDCQPRAFYLKAHSSPDLD SGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYDLDT

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 808-828

**N-glycosylation site.**

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,  
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

**Glycosaminoglycan attachment site.**

amino acids 886-890

**Casein kinase II phosphorylation site.**

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,  
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,  
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,  
1073-1077, 1079-1083, 1081-1085

**Tyrosine kinase phosphorylation site.**

amino acids 667-675

**N-myristoylation site.**

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,  
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

**Leucine zipper pattern.**

amino acids 58-80, 65-87

## FIGURE 107

CAAAACTTTCGCTCGCGGAGAGCGCCAGCTTGACTTGAATGGAAGGAGCCCGAGCCCGCGGAGCGCAGCTGAGAC  
TGGGGGAGCGCGTTTCGGCCTGTGGGGCGCCGCTCGGCGCCGGGGCGCAGCAGGGAAGGGGAAGCTGTGGTCTGCC  
CTGGTCCACGAGGCGCCACTGGTGTGAACCGGAGAGCCCTGGGTGGTCCCGTCCCTATCCCTCCTTTATATA  
GAAACCTTCCACACTGGGAAGGCAGCGCGAGGCGAGGAGGGCTCATGGTGAGCAAGGAGGCCGCTGATCTGCAG  
GCGCACAGCATTCCGAGTTTACAGATTTTACAGATACCAAATGGAAGGCGAGGAGGCAGAACAGCCTGCCTGGT  
TCCATCAGCCCTGGCGCCCAGGCGCATCTGACTCGGCACCCCTGCAGGCACCATGGCCCAGAGCCGGGTGCTGC  
TGCTCCTGCTGCTGCTGCCGCCACAGCTGCACCTGGGACCTGTGCTTGCCGTGAGGGCCCCAGGATTTGGCCGAA  
GTGGCGGCCACAGCCTGAGCCCCGAAGAGAACGAATTTGCGGAGGAGGAGCCGGTGCTGGTACTGAGCCCTGAGG  
AGCCCGGGCCTGGCCCAGCCGCGGTGAGCTGCCCCGAGACTGTGCCTGTTCCAGGAGGGCGTCTGGACTGTG  
GCGGTATTGACCTGCGTGAGTTCCCGGGGACCTGCCCTGAGCACCAACCACCTATCTCTGCAGAACCAACCAG  
TGAAAAAGATCTACCTGAGGAGCTCTCCCGGTGCACCGGCTGGAGACACTGAACCTGCAAAAACAACCGCTGA  
CTTCCCGAGGGCTCCAGAGAAGGCGTTTGGAGCATCTGACCAACCTCAATTACCTGTACTTGGCCAATAACAAGC  
TGACCTTGGCACCCCGCTTCTGCGCAAACGCCCTGATCAGTGTGGACTTTGCTGCCAACTATCTCACCAAGATCT  
ATGGGCTCACCTTTGGCCAGAAGCCAACTTGAGGTCTGTGTACCTGCACAAACAAGCTGGCAGACGCCGGGC  
TGCCGGACAACATGTTCAACGGCTCCAGCAACGTGAGGTCTCATCTGTCCAGCAACTTCTGCGCCACGTGC  
CCAAGCACCTGCCGCTGCCCTGTACAAGCTGCACCTCAAGAACAACAAGCTGGAGAAGATCCCCCGGGGGCCT  
TCAGCGAGCTGAGCAGCCTGCGCGAGCTATACCTGCAGAACCACTACCTGACTGACGAGGGCCTGGACAACGAGA  
CCTTCTGGAAGCTCTCCAGCCTGGAGTACCTGGATCTGTCCAGCAACAACCTGTCTCGGGTCCAGCTGGGCTGC  
CGCGCAGCCTGGTGTCTGCTGCACTTGGAGAAGAAGCCATCCGGAGCGTGGACGCGAATGTGCTGACCCCCATCC  
GCAGCCTGGAGTACCTGCTGCTGCACAGCAACCAGCTGCGGGAGCAGGGCATCCACCCACTGGCCTTCCAGGGCC  
TCAAGCGGTGACACGGTGCACCTGTACAACAACGCGCTGGAGCGCGTGGCCAGTGGCCTGCCTGCGCGGTGC  
GCACCTCATGATCCTGCACAACCAGATCACAGGCATTGGCCGCGAAGACTTTGCCACCACCTACTTCTGGAGG  
AGCTCAACCTCAGCTACAACCGCATCACAGCCACAGGTGCACCGGACGCTTCCGCAAGCTGCGCCTGTCTGC  
GCTCGCTGGACCTGTGCGGCAACCGGTGCACACGCTGCCACCTGGGCTGCCTCGAAATGTCCATGTGCTGAAGG  
TCAAGCGCAATGAGCTGGCTGCCCTTGGCACGAGGGGCGTGGCGGGCATGGCTCAGCTGCGTGAGCTGTACCTCA  
CCAGCAACCGACTGCGCAGCCGAGCCCTGGGCCCCCGTGCCTGGGTGGACCTCGCCCATCTGCAGCTGCTGGACA  
TCGCCGGGAATCAGCTCACAGAGATCCCCGAGGGGCTCCCCGAGTCACTTGAGTACCTGTACCTGCAGAACAA  
AGATTAGTGCAGTGCAGGCTGCGGCAATGCCTTTCGACTCCACGCCCAACCTCAAGGGGATCTTTCTCAGGTTTAA  
TGGCTGTGGGCTCCGTGGTGGACAGTGCTTCCGGAGGCTGAAGCACCTGCAGGTCTTGGACATTGAAGGCAACT  
TAGAGTTTGGTGACATTTCCAAGGACCGTGGCCGCTTGGGGAAGGAAAAGGAGGAGGAGGAAGAGGAGGAGGAGG  
AGGAAGAGGAAACAAGAAGTGAAGTGAAGTGTGACCTAGGATGATGGACCGCCGGACTCTTTTCTGC  
AGCACACGCTGTGTGCTGTGAGCCCCCACTCTGCCGTGCTCACACAGACACACCCAGCTGCACACATGAGGCA  
TCCCACATGACACGGGCTGACACAGTCTCATATCCCCACCCCTTCCACGGCGTGTCCACGGCCAGACACATGC  
ACACACATCACACCTCAAACACCCAGCTCAGCCACACACAACTACCTTCAAACCAACACAGTCTCTGTACAC  
CCCCACTACCGCTGCCACGCCCCTCTGAATCATGCAGGGAAGGGTCTGCCCTTGGCTGGCACACACAGGCACCCA  
TTCCCTCCCCCTGCTGACATGTGTATGCGTATGCATACACACCACACACACACATGCACAAGTCATGTGCGAA  
CAGCCCTCAAAGCCTATGCCACAGACAGCTCTTGGCCAGCCAGAATCAGCCATAGCAGCTCGCCGTCTGCCCT  
GTCCATCTGTCCGTCCGTTCCTTGGAGAAGACACAAGGGTATCCATGCTCTGTGGCCAGGTGCCTGCCACCTCT  
GGAATCACAAAAGCTGGCTTTTATTTCTTTCCATCTATGGGGACAGGAGCCTTCAGGACTGCTGGCCTGGCC  
TGGCCACCTGCTCCTCCAGGTGCTGGGCAGTCACTCTGCTAAGAGTCCCTCCCTGCCACGCCCCTGGCAGGACA  
CAGGCAC'TTTTCCAATGGGCAAGCCAGTGGAGGACAGGATGGGAGAGCCCCCTGGGTGCTGCTGGGGCCTTGGGG  
CAGGAGTGAAGCAGAGGTGATGGGGCTGGGCTGAGCCAGGAGGAAGGACCCAGCTGCACCTAGGAGACACCTTT  
GTTCTTCAAGGCTGTGGGGGAAGTTCGGGTGCCCTTATTTTATTTCTTTCTAAGGAAAAAATGATAAAAAAT  
CTCAAAGCTGATTTTCTTGTATAGAAAACTAATATAAAAGCATTATCCCTATCCCTGCAAAAAA

## **FIGURE 108**

MEGEEAEQPAWFHQPWPGASDSAPPAGTMAQSRVLLLLLLLLPPQLHLGPVLAVRAPGFGRS  
GGHSLSPEENEFAEEEPVLVLSPEEPGPGPAAVSCPRDCACSQEGVDCGGIDLREFPGDLP  
EHTNHLSQLNNQLEKIYPEELSRHLRLETNLQNNRLTSRGLPEKAFEHLTNLNYLYLANNK  
LTLAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV  
EVLILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN  
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLTPIRSLEYLLLHSN  
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMLHNQITGIGREDFATTYF  
LEELNLSYNRITSPQVHRDAFRKLRLRLSLDLSGNRLHTLPPGLPRNVHVLKVKRNELAALA  
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL  
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKD  
RGRLGKEKEEEEEEEEEEEETR

### **Signal sequence:**

amino acids 1-48

### **N-glycosylation site.**

amino acids 243-247, 310-314, 328-332, 439-443

### **Casein kinase II phosphorylation site.**

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

### **N-myristoylation site.**

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,  
477-483, 498-502, 539-545, 548-554

### **Leucine zipper pattern.**

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,  
535-557



[illegible][illegible]

## **FIGURE 110**

MDFLLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP  
RCKHGEICIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD  
GSCSSALTCSMANCQYGCDVVKGQIRCQCPSPLHLAPDGRTCVDVDECATGRASCPRFRQC  
VNTFGSYICKCHKGFDLMYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG  
DGLTCVYIPKVMIEPSGPIHVPKGNLILKGDITGNNNWIPDVGSTWWPPKTPYIPPIITNRP  
TSKPTTRPTPKPTPIPTPPPPPLPTELRTPLPPTTPPERPTTGLTTIAPAASTPPGGITVDN  
RVQTDPOKPRGDVFSVLVHSCNFDHGLCGWIREKDNDLHWEPIRDPAGGQYLTVSAAKAPGG  
KAARLVLPGLRLMHSGDLCLSFHVKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQI  
TLRGADIKSESQR

### **Signal sequence:**

amino acids 1-17

### **N-glycosylation site.**

amino acids 273-277

### **Casein kinase II phosphorylation site.**

amino acids 166-170, 345-349

### **Tyrosine kinase phosphorylation site.**

amino acids 199-206

### **N-myristoylation site.**

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,  
421-427, 433-439, 462-468, 476-482

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 104-116, 186-198, 231-243

### **Cell attachment sequence.**

amino acids 382-385

### **EGF-like domain cysteine pattern signature.**

amino acids 75-87

## FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTTGCCCTTTAGATTGTGA  
AATGTGGCTCAAGGTCTTCACAACCTTTCTTTCTTTTGCAACAGGTGCTTGCTCGGGGCTGA  
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAGGCCCTCTACCTACCCGTC  
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCCA  
CACAATGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCTTGACTTGGAATACC  
AACACAAGTTCACCATGATGCCACCCAATGCATCTCTGCTTATCAACCCACTGCAGTTCCTT  
GATGAAGGCAATTACATCGTGAAGGTCAACATTCAAGGAAATGGAACCTCTATCTGCCAGTCA  
GAAGATACAAGTCACGGTTGATGATCCTGTCAAAAGCCAGTGGTGCAGATTCTCTCTCCCT  
CTGGGGCTGTGGAGTATGTGGGAACATGACCTTGACATGCCATGTGGAAGGGGGCACTCGG  
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC  
TCCCCAAAACAATACCTTTTATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT  
GCCTGGTGAGGAACCTGTCACTGAAATGGAAAGTGATATCATTATGCCCATCATATATTAT  
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTTTACTGT  
TGACCTTGGAGAGGCCATCCTATTTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT  
CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAGCATGGGCCTCGCTTAGAAGTT  
GCATCTGAGAAAGTAGCCCAGAAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAAC  
CGGCAGGCAAGATGAAACTCATTTTACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTG  
CACAGAAAGGAAAATCATTGTACCTTTAGCAAGTATAACTGGAATATCACTATTTTTTGATT  
ATATCCATGTGTCTTCTCTTCTATGGAAAAAATATCAACCCTACAAAGTTATAAAACAGAA  
ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAAGCTCAAACATTTTTCAGGCCATGAAGATG  
CTCTGGATGACTTCGGAATATATGAATTTGTTGCTTTTCCAGATGTTTCTGGTGTTCAGG  
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATCGGGGCAAGATTTGCACAGTACAGT  
GTATGAAGTTATTCAGCACATCCCTGCCCAGCAGCAAGACCATCCAGAGTGAACCTTTCATGG  
GCTAAACAGTACATTTCGAGTGAAATTCTGAAGAAACATTTTAAGGAAAAACAGTGGAAAAGT  
ATATTAATCTGGAATCAGTGAAGAAACAGGACCAACACCTCTTACTCATTATTCCTTTACA  
TGCAGAATAGAGGCATTTATGCAAATTGAACTGCAGGTTTTTCAGCATATACACAATGTCTT  
GTGCAACAGAAAAACATGTTGGGGAAATATTCTCAGTGGAGAGTCGTTCTCATGCTGACGG  
GGAGAACGAAAGTGACAGGGGTTTCTCATAAGTTTTGTATGAAATATCTCTACAAACCTCA  
ATTAGTTCTACTCTACACTTTTCACTATCATCAACACTGAGACTATCCTGTCTCACCTACAAA  
TGTGGAACTTTACATTGTTTCGATTTTTTTCAGCAGACTTTGTTTTATTAAATTTTTATTAGTG  
TTAAGAATGCTAAATTTATGTTTCAATTTTATTTCCAAATTTCTATCTTGTTATTTGTACAA  
CAAAGTAATAAGGATGGTTGTCAAAAAACAAAACCTATGCCTTCTCTTTTTTTTCAATCACC  
AGTAGTATTTTTTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTTTTTA  
TTTTTTTCAAGGAAAGATGGATTCAAATAAATTATTCTGTTTTTGCTTTTAAAAAAAAAAAAAA

## **FIGURE 112**

MWLKVFTTFLSFATGACSGLKVTVPSTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH  
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGTLSASQ  
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNRPFVHTSSTYSFS  
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNSDKGLKVGEVFTV  
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNIT  
GRQDETHFTVIIITSVGLEKLAQKGKSLSPASITGISLFLIISMCLLFLWKKYQPYKVIKQK  
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRVSPASDCVSGQDLHSTV  
YEVIQHIIPAQQQDHPE

### **Signal sequence:**

amino acids 1-18

### **Transmembrane domain:**

amino acids 341-359

### **N-glycosylation site.**

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,  
276-280, 308-312

### **Casein kinase II phosphorylation site.**

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

### **Tyrosine kinase phosphorylation site.**

amino acids 272-280

### **N-myristoylation site.**

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,  
239-245

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## FIGURE 113

GCAAGCGGCGAAATGCGGCCCTCCGGGAGTCTTGCAAGTTCCTGGCAGTCCTGGTGCTGTT  
GCTTTGGGGTGCTCCCTGGACGCACGGGCGGCGGAGCAACGTTTCGCGTCATCACGGACGAGA  
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTTATGCCCCGTGGTGCCCTGCT  
TGTCAAAATCTTCAACCGGAATGGGAAAGTTTTGCTGAATGGGGAGAAGATCTTGAGGTTAA  
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTTATCATAACTGCTC  
TTCCTACTATTTATCATTTGTAAGATGGTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAG  
AAGGACTTCATAAACTTTATAAGTGATAAAGAGTGGAAGAGTATTGAGCCCGTTTCATCATG  
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTTCAGCTATCTATGTGGA  
TCAGGACGTGCCATAACTACTTTATTGAAGACCTTGGATTGCCAGTGTGGGGATCATATACT  
GTTTTTGCTTTAGCAACTCTGTTTTCCGGACTGTTATTAGGACTCTGTATGATATTTGTGGC  
AGATTGCCTTTGTCTTCAAAAAGGCGCAGACCACAGCCATACCCATACCCCTTCAAAAAAAT  
TATTATCAGAATCTGCACAACCTTTGAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA  
GATGTTTCAGAAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTTCCACAGAATGC  
CATAAGACAACGCTCTCTGGGTCCATCATTGGCCACAGATAAATCCTAGTTAAATTTTATAG  
TTATCTTAATATTATGATTTTGATAAAAAACAGAAGATTGATCATTTTGTTTGGTTTGAAGTG  
AACTGTGACTTTTTTGAATATTGCAGGGTTCAGTCTAGATTGTCATTAAATTGAAGAGTCTA  
CATTGAGAACATAAAAGCACTAGGTATACAAGTTTGAAATATGATTTAAGCACAGTATGATG  
GTTTAAATAGTTCTCTAATTTTTGAAAAATCGTGCCAAGCAATAAGATTTATGTATATTTGT  
TTAATAATAACCTATTTCAAGTCTGAGTTTTGAAAATTTACATTTCCCAAGTATTGCATTAT  
TGAGGTATTTAAGAAGATTATTTTAGAGAAAAATATTTCTCATTTGATATAATTTTTCTCTG  
TTTCACTGTGTGAAAAAAGAAGATATTTCCCATAAATGGGAAGTTTGCCCATTTGTCTCAAG  
AAATGTGTATTTTCAGTGACAATTTCTGGTCTTTTTTAGAGGTATATTCCAAATTTCTTGT  
ATTTTTAGGTTATGCAACTAATAAAAACTACCTTACATTAATTAATTACAGTTTTCTACACA  
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTTTTAAGTTCATGGTATTCTCTTGATTC  
CAACAAAGTTTGATTTTCTCTTGATTTTTTCTTACTTACTATGGGTACATTTTTTATTTTT  
CAAATTGGATGATAATTTCTTGAAACATTTTTTATGTTTTAGTAAACAGTATTTTTTTGTT  
GTTTCAAACCTGAAGTTTACTGAGAGATCCATCAAATTGAACAATCTGTTGTAATTTAAAT  
TTGGCCACTTTTTTCAGATTTTACATCATTCTTGCTGAACCTTCAACTTGAAATTGTTTTTT  
TTTCTTTTTGGATGTGAAGGTGAACATTCCTGATTTTTGTCTGATGTGAAAAAGCCTTGGA  
TTTTACATTTTGAAAATTCAAAGAAGCTTAATATAAAAGTTTGCATTCTACTCAGGAAAAAG  
CATCTTCTTGATATATGTCTTAAATGTATTTTTGTCCTCATATACAGAAAGTTCTTAATTGAT  
TTTACAGTCTGTAATGCTTGATGTTTTAAATAATAACATTTTATATTTTTTAAAAGACAA  
ACTTCATATTATCCTGTGTTCTTTCTGACTGGTAATATTGTGTGGGATTTACAGGTAAAA  
GTCAGTAGGATGGAACATTTTAGTGATTTTTTACTCCTTAAAGAGCTAGAATACATAGTTTT  
CACCTTAAAAGAAGGGGAAAATCATAAATACAATGAATCAACTGACCATTACGTAGTAGAC  
AATTTCTGTAATGTCCCTTCTTTCTAGGCTCTGTTGCTGTGTGAATCCATTAGATTTACAG  
TATCGTAATATACAAGTTTTCTTTAAAGCCCTCTCCTTTAGAATTTAAATATTGTACCATT  
AAAGAGTTTGGATGTGTAACCTGTGATGCCTTAGAAAAATATCCTAAGCACAAAATAAACCT  
TTCTAACCACTTCATTAAAGCTGAAAAAAAAAAAAAAAAA

[illegible]

MAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL  
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIIITALPTIYHCKDGEFRRYQGPRTKKDFI  
NFI~~SD~~KEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL  
ATLFSGLLLGLCMIFVADCLCPSKRRRPQPYPYPSKKLLSESAQPLKKVEEEQEAEDEEDVSE  
EEAESKEGTNKDFPONAIRORSLGPSLATDKS

**Signal sequence:**

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

## FIGURE 115

GCGAGTGTCCAGCTGCGGAGACCCGTGATAATTCGTAACTAATTCAACAAACGGGACCCCTT  
CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGGACAGGCGGATTGGAAGAGCGGG  
AAGGTCCTGGCCCAGAGCAGTGTGACACTTCCCTCTGTGACCATGAAACTCTGGGTGTCTGC  
ATTGCTGATGGCCTGGTTTGGTGTCTTGAGCTGTGTGCAGGCCGAATTCTTCACCTCTATTG  
GGCAGATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC  
CTTGTGGAGGAAGCCAAGCTTTCAGAGATTAAGAGCTGGGCCAACAAAATGGAAGCCTTGAC  
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAACTGG  
TGAAGCGGCTAAACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGCAGGACTCAGCTGCA  
GGTTTTATCGCCAACCTCTCTGTGCAGCGGCAGTTCTTCCCCACTGATGAGGACGAGATAGG  
AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTTCCA  
GAGGGGAACTTCCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATG  
GGCCGCTCGGCCTACAATGAAGGGGACTATTATCATAACGGTGTGTGGATGGAGCAGGTGCT  
AAAGCAGCTTGATGCCGGGGAGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCA  
GCTATGCTGTCTTCCAGTTGGGTGATCTGCACCGTGCCCTGGAGCTCACCCGCCGCTGCTC  
TCCCTTGACCCAAGCCACGAACGAGCTGGAGGGAATCTGCGGTACTTTGAGCAGTTATTGGA  
GGAAGAGAGAGAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCCAAGAGGCA  
TCTATGAGAGGCCTGTGGACTACCTGCCTGAGAGGGATGTTTACGAGAGCCTCTGTCTGTTGG  
GAGGGTGTCAAACCTGACACCCCGTAGACAGAAGAGGCTTTTCTGTAGGTACCACCATGGCAA  
CAGGGCCCCACAGCTGCTCATTTGCCCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCGCACA  
TCGTCAGGTACTACGATGTCTGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA  
CCTAAACTTGCACGAGCCACCGTTCTGTGATCCCAAGACAGGAGTCTCACTGTGCGCCAGCTA  
CCGGGTTTCCAAAAGCTCCTGGCTAGAGGAAGATGATGACCCTGTTGTGGCCCGAGTAAATC  
GTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAAAT  
TATGGAGTGGGAGGACAGTATGAACCGCACTTCGACTTCTCTAGGCGACCTTTTGACAGCGG  
CCTCAAAACAGAGGGGAATAGGTTAGCGACGTTTCTTAACTACATGAGTGTGTAGAAGCTG  
GTGGTGCCACCGTCTTCCCTGATCTGGGGGCTGCAATTTGGCCTAAGAAGGGTACAGCTGTG  
TTCTGGTACAACCTCTTGCGGAGCGGGGAAGGTGACTACCGAACAAGACATGCTGCCTGCC  
TGTGCTTGTGGGCTGCAAGTGGGTCTCCAATAAGTGGTTCCATGAACGAGGACAGGAGTTCT  
TGAGACCTTGTGGATCAACAGAAGTTGACTGACATCCTTTTCTGTCTTCCCCTTCCTGGTC  
CTTCAGCCCATGTCAACGTGACAGACACCTTTGTATGTTTCTTTGTATGTTTCTATCAGGCT  
GATTTTTTGGAGAAATGAATGTTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT  
GTGACTGAAGTCCCAGCCCTTCATTTCAGCCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA  
AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCTTTGTACCTCAGGTGTT  
TTAGGTGTGAGATGTTTCAGTGAACCAAAGTTCTGATACCTTGTTTACATGTTTGTGTTTTAT  
GGCATTTCTATCTATTGTGGCTTTACCAAAAAATAAAATGTCCCTACCAGAAAAA

## **FIGURE 116**

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA  
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALDVLQDSAAGFIANLSVQRQFFP  
TDEDEIGAALKMRLQDTYRLDPGTISRGLPGTKYQAMLSVDDCFGMGRSAYNEGDYYHTV  
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRLLSLDPSHERAGGNLR  
YFEQLLEEEEREKTLTNQTEAELATPEGIYERPDYLPERDVYESLCRGEVGLTPRRQKRLF  
CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYDVMSEDEIERIKEIAKPKLARATVRDPKTG  
VLTVASYRVSKSSWLEEDDDPVVARVNRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS  
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEGDYR  
TRHAACPVLVGCKWVSNKWFHERGQEFRLPCGSTVD

### **Signal sequence:**

amino acids 1-17

### **N-glycosylation site.**

amino acids 115-119, 264-268

### **Glycosaminoglycan attachment site.**

amino acids 490-494

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 477-481

### **Casein kinase II phosphorylation site.**

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,  
346-350, 365-369, 385-389, 457-461, 530-534

### **Tyrosine kinase phosphorylation site.**

amino acids 71-80, 489-496

### **N-myristoylation site.**

amino acids 14-20, 131-137, 171-177, 446-452

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 8-19

### **Leucine zipper pattern.**

amino acids 213-235



## FIGURE 117

GCAGTATTGAGTTTTACTTCCTCCTCTTTTTAGTGGAAGACAGACCATAATCCCAGTGTGAGTGAAATTGATTGT  
TTCATTTATTACCGTTTTGGCTGGGGGTAGTTCCGACACCTTCACAGTTGAAGAGCAGGCAGAAGGAGTTGTGA  
AGACAGGACAATCTTCTTGGGGATGCTGGTCTGGAAGCCAGCGGGCCTTGCTCTGTCTTTGGCCTCATTGACCC  
CAGGTTCTCTGGTTAAAACTGAAAGCCTACTACTGGCCTGGTGCCCATCAATCCATTGATCCTTGAGGCTGTGCC  
CCTGGGGCACCCACCTGGCAGGGCCTACCACCATGCGACTGAGCTCCCTGTTGGCTCTGCTGCGGGCCAGCGCTTC  
CCCTCATCTTAGGGCTGTCTCTGGGGTGACGCTGAGCCTCCTGCGGGTTTCTTGGATCCAGGGGGAGGGAGAAG  
ATCCCTGTGTGAGGCTGTAGGGGAGCGAGGAGGGCCACAGAATCCAGATTGAGAGCTCGGCTAGACCAAAGTG  
ATGAAGACTTCAAACCCCGATTGTCCCCTACTACAGGGACCCCAACAAGCCCTACAAGAAGGTGCTCAGGACTC  
GGTACATCCAGACAGAGCTGGGCTCCCGTGAGCGGTTGCTGGTGGCTGTCTGACCTCCCGAGCTACACTGTCCA  
CTTTGGCCGTGGCTGTGAACCGTACGGTGGCCCATCACTTCCCTCGGTACTCTACTTCACTGGGCAGCGGGGG  
CCCGGGCTCCAGCAGGGATGCAGGTGGTGTCTCATGGGGATGAGCGGCCCGCCTGGCTCATGTGAGAGACCTGC  
GCCACCTTCACACACACTTTGGGGCCGACTACGACTGGTTCTTCATCATGCAGGATGACACATATGTGCAGGCCC  
CCCGCCTGGCAGCCCTTGCTGGCCACCTCAGCATCAACCAAGACCTGTACTTAGGCCGGGCAGAGGAGTTTATTG  
GCGCAGGCGAGCAGGCCCGGTACTGTGATGGGGCTTTGGCTACCTGTTGTACGGAGTCTCCTGCTTCGTCTGC  
GGCCACATCTGGATGGCTGCCGAGGAGACATTCTCAGTGCCCGTCTGACGAGTGGCTTGGACGCTGCCCTATTG  
ACTCTCTGGGCGTCGGCTGTGTCTCACAGCACCAGGGGCAGCAGTATCGCTCATTTGAATGGCCAAAAATAGGG  
ACCTTGAGAAGGAAGGGAGCTCGGCTTTCTGAGTGCCTTCGCCGTGCACCCCTGTCTCCGAAGGTACCCCTCATGT  
ACCGGCTCCACAAACGCTTCAGCGCTCTGGAGTTGGAGCGGGCTTACAGTGAATAGAACAACATGCAGGCTCAGA  
TCCGGAACCTGACCGTGCTGACCCCCGAAGGGGAGGCAGGGCTGAGCTGGCCCGTTGGGCTCCCTGCTCCTTTCA  
CACCACACTCTCGCTTTGAGGTGCTGGGCTGGGACTACTTCACAGAGCAGCACACCTTCTCCTGTGCAGATGGGG  
CTCCCAAGTGCCCACTACAGGGGGCTAGCAGGGCGGACGTGGGTGATGCGTTGGAGACTGCCCTGGAGCAGCTCA  
ATCGGCGCTATCAGCCCCGCTGCGCTTCAGAAGCAGCGACTGCTCAACGGCTATCGGCGCTTCGACCCAGCAC  
GGGGCATGGAGTACACCTGGACCTGCTGTTGGAATGTGTGACACAGCGTGGGCACCGCGGGCCCTGGCTCGCA  
GGGTGAGCCTGCTGCGGCCACTGAGCCGGGTGGAAATCCTACCTATGCCCTATGTCACTGAGGCCACCCGAGTGC  
AGCTGGTGCTGCCACTCCTGGTGGCTGAAGCTGCTGCAGCCCCGGCTTTCTCGAGGCGTTTGCAGCCAATGTCC  
TGGAGCCACGAGAATGCAATTGCTCACCTGTTGCTGGTCTACGGGCCACGAGAAGGTGGCCGTGGAGCTCCAG  
ACCCATTTCTTGGGGTGAAGGCTGCAGCAGCGGAGTTAGAGCGACGGTACCCCTGGGACGAGGCTGGCCTGGCTCG  
CTGTGCGAGCAGAGGCCCCCTTCCAGGTGCGACTCATGGACGTGGTCTCGAAGAAGCACCCCTGTGGACACTCTCT  
TCTTCCTTACCACCGTGTGGACAAGGCCTGGGCCCGAAGTCTCAACCGCTGTGCGATGAATGCCATCTCTGGCT  
GGCAGGCCTTCTTTCCAGTCCATTTCCAGGAGTTCAATCCTGCCCTGTACCCACAGAGATCACCCCCAGGGCCCC  
CGGGGGCTGGCCCTGACCCCCCTCCCCTCCTGGTGTGACCCCTCCCGGGGGCTCCTATAGGGGGGAGATTTG  
ACCGGCAGGCTTCTGCGGAGGGCTGCTTCTACAACGCTGACTACCTGGCGGCCCGAGCCCGGCTGGCAGGTGAAC  
TGGCAGGCCAGGAAGAGGAGGAAGCCCTGGAGGGGCTGGAGGTGATGGATGTTTCTCCGGTTCTCAGGGCTCC  
ACCTCTTTGCGGCCGTAGAGCCAGGGCTGGTGAGAAGTTCTCCCTGCGAGACTGCAGCCCACGGCTCAGTGAAG  
AACTCTACCACCGCTGCCGCTCAGCAACCTGGAGGGGCTAGGGGGCCGTGCCAGCTGGCTATGGCTCTCTTTG  
AGCAGGAGCAGGCCAATAGCACTTAGCCCGCCTGGGGGCCCTAACCTCATTACCTTTCTTTGTCTGCCCTCAGCC  
CCAGGAAGGGCAAGGCAAGATGGTGGACAGATAGAGAATTGTTGCTGTATTTTTTAAATATGAAAATGTTATTAA  
ACATGTCTTCTGCC

## **FIGURE 118**

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQEGEDPCVEAVGERGGPQNPD SRARLD  
QSDDFKPRIVPYRDPNKPYPKKVLRTRYIQTELGSRRERLLVAVLTSRATLSTLAVAVNRTV  
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHTHFGADYDWFFIMQDDTY  
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRLLLLRLRPHLDGCRG  
DILSÄRPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE  
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGEAGLSWPVGLPAPFTPHSRFEV  
LGWDYFTEQHTFSCADGAPKCPLOGASRADVGDALETALEQLNRRYQPRLRFOKQRLNNGYR  
RFDPARMEYTLDLLLECVTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATRVQLVLP LL  
VAEAAAAPAFLEAFAANVLEPREHALLTLLL VYGPREGGRGAPDPFLGVKAAAELERRYPG  
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLT TVWTRPGPEVLNRCRMNAISGWQAFFP  
VHFQEFNPALSPQRSPPGPPGAGDPSPSPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA  
RARLAGELAGQEEEEALEGLEVMDFLRFSLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR  
CRLSNLEGLGGRAQLAMALFEQE QANST

### **Signal sequence:**

amino acids 1-15

### **Transmembrane domain:**

amino acids 489-507

### **N-glycosylation site.**

amino acids 121-125, 342-346

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

### **Casein kinase II phosphorylation site.**

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

### **Tyrosine kinase phosphorylation site.**

amino acids 736-743

### **N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-678

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

### **Cell attachment sequence.**

amino acids 247-250

## FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGCTGCGCTTTCCTGTCCCCAAGCC  
GTTCTAGACGCGGGAAAAATGCTTCTGAAAGCAGCTCCTTTTTGAAGGGTGTGATGCTTGG  
AAGCATTTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA  
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAATTTCA  
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTTCGAGTATACTGTATTATCCTTGTAACCA  
CAAAGATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACACTGTGACAAAGCAG  
AGTTCTTCAGTTCTGAAAATGTTAAAGTGTTGAGTCAATTAATATGGACACAAATGACATG  
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTTGATAAGTATAGAGACCAATACAACTG  
GTTCTTCCTTGCACGCCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTGTAA  
AAAAGGATCCATCACAGCCTTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT  
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAAGTCAATGAAAAGACTTAACAGCCTTCT  
CAATATCCCAGAAAAGTGTCCTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAAC  
AGCTAGCAGTTTGCCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGA  
AAAGATGTATTTAATACCAAATCTGTTGGGCTTTCTATTAAAGAGGCAATGACTTATCACCC  
CAACCAGGTAGTAGAAGGCTGTTGTTGAGATATGGCTGTTACTTTTAATGGACTGACTCCAA  
ATCAGATGCATGTGATGATGTATGGGGTATAACGCCTTAGGGCATTTGGGCATATTTTCAAT  
GATGCATTGGTTTTCTTACCTCCAAATGGTTCTGACAATGACTGAGAAGTGGTAGAAAAGCG  
TGAATATGATCTTTGTATAGGACGTGTGTTGTCATTATTTGTAGTAGTAACACATATCCAA  
TACAGCTGTATGTTTCTTTTTCTTTTCTAATTTGGTGGCACTGGTATAACCACACATTAAAG  
TCAGTAGTACATTTTTTAAATGAGGGTGGTTTTTTTTCTTTAAACACATGAACATTGTAAATG  
TGTTGGAAAGAAGTGTTTTAAGAATAATAATTTTGCAAATAAACTATTAATAAATATTATAT  
GTGATAAATTCTAAATTATGAACATTAGAAATCTGTGGGGCACATATTTTTGCTGATTGGTT  
AAAAAATTTTAAACAGGTCTTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT  
TGTGATTAAAGTAAACTTTTAGCTGTGTGTTCCCTTTACTTCTAATACTGATTTATGTTCT  
AAGCCTCCCCAAGTTCCAATGGATTTGCCTTCTCAAAATGTACAATAAGCAACTAAAGAAA  
ATTAAAGTGAAAGTTGAAAAAT

## **FIGURE 120**

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME  
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRK  
AYKYAFDKYRDQYNWFFLARPTTFAI IENLKYFLLKKDPSQPFYLGHTIKSGDLEYVGMEGG  
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFN  
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL  
PPNGSDND

### **Signal sequence:**

amino acids 1-33

### **N-glycosylation site.**

amino acids 121-125, 342-346

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

### **Casein kinase II phosphorylation site.**

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

### **Tyrosine kinase phosphorylation site.**

amino acids 736-743

### **N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-672

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

### **Cell attachment sequence.**

amino acids 247-250

## FIGURE 121

CCCACGCGTCCGATCTTACCAACAAAACACTCCTGAGGAGAAAGAAAGAGAGGGAGGGAGAG  
AAAAAGAGAGAGAGAGAGAAACAAAAAACCAAAGAGAGAGAGAAAAAATGAATTCATCTAAATCAT  
CTGAAACACAATGCACAGAGAGAGGATGCTTCTCTTCCCAAATGTTCTTATGGACTGTTGCT  
GGGATCCCCATCCTATTTCTCAGTGCCTGTTTCATCACCAGATGTGTTGTGACATTTTCGCAT  
CTTTCAAACCTGTGATGAGAAAAAGTTTCAGCTACCTGAGAATTTACAGAGCTCTCCTGCT  
ACAATTATGGATCAGGTTCAAGTCAAGAATTGTTGTCCATTGAACTGGGAATATTTTCAATCC  
AGCTGCTACTTCTTTTCTACTGACACCATTTCTGCGGCTTAAGTTTAAAGAACTGCTCAGC  
CATGGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCCTTTCCTACAAGA  
AACCTAAAATGAGAGAGTTTTTTTATTGGACTGTCAGACCAGGTTGTCGAGGGTCAAGTGGCAA  
TGGGTGGACGGCACACCTTTGACAAAGTCTCTGAGCTTCTGGGATGTAGGGGAGCCCAACAA  
CATAGCTACCCTGGAGGACTGTGCCACCATGAGAGACTCTTCAAACCCAAGGCAAATTTGGA  
ATGATGTAACCTGTTTCCTCAATTATTTTCGGATTTGTGAAATGGTAGGAATAAATCCTTTG  
AACAAAGGAAAATCTCTTTTAAGAACAGAAGGCACAACCTCAAATGTGTAAAGAAGGAAGAGCA  
AGAACATGGCCACACCCACCGCCCCACACGAGAAATTTGTGCGCTGAACTTCAAAGGACTTC  
ATAAGTATTTGTTACTCTGATACAAATAAAAAATAAGTAGTTTAAATGTTAAAAAAAAAAAAA  
AAA  
AAAAA

## **FIGURE 122**

MNSSKSSETQCTERGCFSQMFLLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN  
FTELSYNYGSGSVKNCCPLNWEYFQSSCYFFSTDTISWALSLKNCSAMGAHLVVINSQEEQ  
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPNNIATLEDCATMRDSS  
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

### **Signal sequence:**

amino acids 1-42

### **N-glycosylation site.**

amino acids 2-6, 62-66, 107-111

### **Casein kinase II phosphorylation site.**

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

### **N-myristoylation site.**

amino acids 15-21, 74-80, 155-161

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 27-38

## FIGURE 123

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCCCTCAGCAACCCTCGACATGGCGCTGAGGCGGCCACCGCGAC  
TCCGGCTCTGCGCTCGGCTGCCTGACTTCTTCTGCTGCTGCTTTTCAGGGGCTGCCTGATAGGGGCTGTAAATC  
TCAAAATCCAGCAATCGAACCCAGTGGTACAGGAATTTGAAAGTGTGGAACCTGTCTTGATCATATTACGGATTTCGC  
AGACAAGTGACCCAGGATCGAGTGGAAAGAAAATTCAGATGAACAAACCACATATGTGTTTTTTGACAACAAAA  
TTCAGGGAGACTTGGCGGGTCTGTCAGAAATACTGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG  
ACTCAGCCCTTTATCGCTGTGAGGTCTTGTCTGAAATGACCGCAAGGAAATTGATGAGATTGTGATCGAGTTAA  
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCCGAAGGCTGTACCAGTAGGCAAGATGGCAACACTGC  
ACTGCCAGGAGAGTGAGGGCCACCCCGGCCCTCACTACAGCTGGTATCGCAATGATGTACCCTGCCCACGGATT  
CCAGAGCCAATCCCAGATTTTCGCAATTCTTCTTTCCACTTAAACTCTGAAACAGGCAC'TTTGGTGTTCAC'TGCTG  
TTCACAAGGACGACTCTGGGCACTACTACTGCATTGCTTCCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG  
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGGTTCTGGTTGTCCTTGCTGTACTGGCCCTGA  
TCACGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA  
ACCCAGGGAAACCAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCGACTTCAGACACAAGTCATCGTTTG  
TGATCTGAGACCCGCGGTGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAACTCCTGTCAA  
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATT'CAGAAGCTTTTCGTTTTGGCCAAAGTTGACCA  
CTACTCTTCTTACTCTAACAAGCCACATGAATAGAAGAATTTTCTCAAGATGGACCCGGTAAATATAACCACAA  
GGAAGCGAAACTGGGTGCGTTCACTGAGTTGGGTTCCATACTGTTTCTGGCCTGATTCCCGCATGAGTATTAGG  
GTGATCTTAAAGAGTTTGTCTCAGTAAACGCCCGTGTGGGCCCTGTGAAGCCAGCATGTTCACTACTGGTCTGTT  
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCCGGCGGGAACCCA  
GAAAAGGCTTCTTACACAGCAGCCTTACTTCATCGGCCACAGACACCACCGCAGTTTCTTCTTAAAGGCTCTGC  
TGATCGGTGTTGCACTGTCCATTGTGGAGAAGCTTTTTGGATCAGCATTTTGTAAAAACAACCAAAATCAGGAAG  
GTAAATTGGTGTGCTGGAAGAGGGATCTTGCCCTGAGGAACCTGCTTGTCCAACAGGCTGTGAGGATTTAAGGAAA  
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTTCTATGGGTCTTGTATTATTTATATAAATTT  
TACATCTAAATTTTTGCTAAGGATGTATTTTGAATTATTGAAAAGAAAATTTCTATTTAACTGTAAATATATTGT  
CATACAATGTAAATAACCTATTTTTTTAAAAAAGTTCAACTTAAGGTAGAAGTTCCAAGCTACTAGTGTTAAAT  
TGGAAAATATCAATAATTAAGAGTATTTTACCCAAGGAATCCTCTCATGGAAGTTTACTGTGATGTTCCTTTTCT  
CACACAAGTTTTAGCCTTTTTTCAAGGGAACCTCATACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT  
TAAAAATTCAGTTAAGCAATGTTGAAATCAGTTTGCATCTCTTCAAAAGAAACCTCTCAGGTTAGCTTTGAACT  
GCCTCTTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACACAGATG  
CCAGTCAGCTCCTGGGGTTGCGCCAGGCGCCCCGCTCTAGCTCACTGTTGCCTCGCTGTCTGCCAGGAGGCCCT  
GCCATCCTTGGGCCCTGGCAGTGGCTGTGTCCAGTGAGCTTTACTCACGTGGCCCTTGCTTCATCCAGCACAGC  
TCTCAGGTGGGCACTGCAGGGACACTGGTGTCTTCCATGTAGCGTCCAGCTTTGGGCTCCTGTAACAGACCTCT  
TTTTGGTTATGGATGGCTCACAAAATAGGGCCCCCAATGCTATTTTTTTTTTTAAGTTTGTTTAATTATTTGTT  
AAGATTGTCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAAGTACAATAACATTTTTTAAAGAAAAATGGAT  
CCCACTGTTCTCTTTGCCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTGCGATTTCAAAACAAACCATGAT  
GGAGTGGCGGCCAGTCCAGCCTTTTAAAGAACGTCAGGTGGAGCAGCCAGGTGAAAGGCCCTGGCGGGGAGGAAAG  
TGAAACGCCTGAATCAAAAGCAGTTTTCTAATTTTGACTTTAAATTTTTCATCCGCCGGAGACACTGCTCCCAT  
TGTGGGGGGACATTAGCAACATCACTCAGAAGCCTGTGTTCTTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT  
GCCGTGCTGGACTCAGGACTGAAGTGCTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCCCTGGA  
GAATGGCTCTCACTACTCACCTTGTCTTTAGCTTCCAGTGTCTTGGGTTTTTTTATCTTTGACAGCTTTTTTTT  
AATTGCATACATGAGACTGTGTTGACTTTTTTTAGTTATGTGAAACACTTTGCCGCAGGCCGCTGGCAGAGGCA  
GGAAATGCTCCAGCAGTGGCTCAGTGCTCCCTGGTGTCTGCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTC  
CCTCCATCATTGCCACCTTGGTAGAGAGGGATGGCTCCCCACCCTCAGCGTTGGGGATTACAGCTCCAGCCTCCT  
TCTTGGTTGTATAGTGATAGGGTAGCCTTATTGCCCCCTCTTCTTATACCTTAAACCTTCTACACTAGTGCCA  
TGGGAACCAGGTCTGAAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA  
CGGAAAAGGAATACTCGTGATTTTTAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT  
GCCTTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTAATAACACACCCGTAATTTGGCATTTGTTTAA  
CTCATTTATAAAAGCTTCAAAAAACCCA

## **FIGURE 124**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624

><subunit 1 of 1, 310 aa, 1 stop

><MW: 35020, pI: 7.90, NX(S/T): 3

MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS  
PRIEWKKIQDEQTTYVFFDNKIQGLAGRAEILGKTS�KIWNVTRRDSALYRCEVVARNDRK  
EIDEIVIELTVQVKPVTVCRVKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA  
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDLNIIGGIIG  
VLVVLAVLALITLGICCAYYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-30

#### **Transmembrane domain:**

amino acids 243-263

#### **N-glycosylation sites.**

amino acids 104-107, 192-195

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

#### **Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

#### **Tyrosine kinase phosphorylation site.**

amino acids 69-77

#### **N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267